GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 19:21:19 ; Search time 25 Seconds
(without alignments)
549.620 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2391	100.0	467	2	US-08-967-101-2	Sequence 2, Appli
2	2391	100.0	467	2	US-08-592-541-2	Sequence 2, Appli
3	2391	100.0	467	3	US-09-124-698-2	Sequence 2, Appli
4	2391	100.0	467	4	US-09-127-480-2	Sequence 2, Appli
5	2391	100.0	467	4	US-08-496-841C-2	Sequence 2, Appli
6	2391	100.0	467	4	US-09-124-523-2	Sequence 2, Appli
7	2387	99.8	467	2	US-08-967-101-134	Sequence 134, App
8	2387	99.8	467	2	US-08-592-541-134	Sequence 134, App
9	2387	99.8	467	3	US-08-923-454A-10	Sequence 10, Appl
10	2387	99.8	467	3	US-08-670-964-2	Sequence 2, Appli
11	2387	99.8	467	3	US-08-888-077A-2	Sequence 2, Appli
12	2387	99.8	467	3	US-09-124-698-134	Sequence 134, App
13	2387	99.8	467	4	US-09-127-480-134	Sequence 134, App
14	2387	99.8	467	4	US-08-496-841C-134	Sequence 134, App
15	2387	99.8	467	4	US-08-832-867-3	Sequence 3, Appli
16	2387	99.8	467	4	US-09-227-725A-1	Sequence 1, Appli
17	2387	99.8	467	4	US-09-124-523-134	Sequence 134, App
18	2387	99.8	467	4	US-09-375-318-3	Sequence 3, Appli
19	2382	99.6	467	4	US-08-706-344C-2	Sequence 2, Appli
20	2377	99.4	467	4	US-08-706-344C-32	Sequence 32, Appl
21	2372	99.2	467	4	US-08-706-344C-30	Sequence 30, Appl
22	2370	99.1	467	4	US-08-706-344C-28	Sequence 28, Appl
23	2361	98.7	463	3	US-08-888-077A-4	Sequence 4, Appli
24	2357	98.6	463	3	US-08-670-964-4	Sequence 4, Appli
25	2355	98.5	467	4	US-08-706-344C-4	Sequence 4, Appli
26	2334	97.6	463	2	US-08-670-479-18	Sequence 18, Appl
27	2300	96.2	462	3	US-08-788-231A-15	Sequence 15, Appl
28	2237	93.6	467	3	US-08-888-077A-17	Sequence 17, Appl
29	2237	93.6	467	4	US-08-496-841C-136	Sequence 136, App
30	2190	91.6	467	2	US-08-967-101-4	Sequence 4, Appli
31	2190	91.6	467	2	US-08-592-541-4	Sequence 4, Appli
32	2190	91.6	467	3	US-09-124-698-4	Sequence 4, Appli
33	2190	91.6	467	4	US-09-127-480-4	Sequence 4, Appli
34	2190	91.6	467	4	US-08-496-841C-4	Sequence 4, Appli
35	2190	91.6	467	4	US-09-124-523-4	Sequence 4, Appli
36	2183.5	91.3	465	3	US-08-788-231A-17	Sequence 17, Appl
37	2066	86.4	407	2	US-08-875-972-4	Sequence 4, Appli
38	1461	61.1	448	2	US-08-967-101-137	Sequence 137, App
39	1461	61.1	448	2	US-08-592-541-137	Sequence 137, App
40	1461	61.1	448	3	US-08-888-077A-19	Sequence 19, Appl
41	1461	61.1	448	3	US-09-124-698-137	Sequence 137, App
42	1461	61.1	448	4	US-09-127-480-137	Sequence 137, App
43	1461	61.1	448	4	US-09-227-725A-2	Sequence 2, Appli
44	1461	61.1	448	4	US-09-124-523-137	Sequence 137, App
45	1461	61.1	448	4	US-09-375-318-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-967-101-2
; Sequence 2, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-967-101-2

Query Match 100.0%; Score 2391; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

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Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
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Db    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
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Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

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Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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RESULT 2
US-08-592-541-2
; Sequence 2, Application US/08592541
; Patent No. 5986054
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-592-541-2

Query Match 100.0%; Score 2391; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
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Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
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Db    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
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Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
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Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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RESULT 3
US-09-124-698-2
; Sequence 2, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-124-698-2

  Query Match             100.0%;  Score 2391;  DB 3;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-235;
  Matches  467;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
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Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
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Db    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
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Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
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Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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RESULT 4
US-09-127-480-2
; Sequence 2, Application US/09127480
; Patent No. 6194153
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  183
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  High Street Tower - 125 High Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/127,480
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/592,541
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-127-480-2

  Query Match             100.0%;  Score 2391;  DB 4;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-235;
  Matches  467;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
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Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
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Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
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Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 5
US-08-496-841C-2
; Sequence 2, Application US/08496841C
; Patent No. 6210919
;   GENERAL INFORMATION:
;        APPLICANT: ST. GEORGE-HYSLOP, PETER H
;                   ROMMENS, JOHANNA M
;                   FRASER, PAUL E
;        TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
;                            TO ALZHEIMER'S DISEASE
;        NUMBER OF SEQUENCES: 175
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Darby & Darby, PC
;             STREET: 805 Third Avenue
;             CITY: New York
;             STATE: New York
;             COUNTRY: U.S.A.
;             ZIP: 10022
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
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;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/496,841C
;             FILING DATE: 28-Jun-1995
;             CLASSIFICATION: <Unknown>
;          ATTORNEY/AGENT INFORMATION:
;             NAME: Paul F. Fehlner, Ph.D.
;             REGISTRATION NUMBER: 35,135
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 527-7700
;             TELEFAX: (212) 753-6237
;    INFORMATION FOR SEQ ID NO: 2:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 467 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-496-841C-2

  Query Match             100.0%;  Score 2391;  DB 4;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-235;
  Matches  467;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 6
US-09-124-523-2
; Sequence 2, Application US/09124523
; Patent No. 6395960
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  183
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  High Street Tower - 125 High Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/124,523
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/592,541
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-124-523-2

  Query Match             100.0%;  Score 2391;  DB 4;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-235;
  Matches  467;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 7
US-08-967-101-134
; Sequence 134, Application US/08967101
; Patent No. 5840540
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
```

```
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  183
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  High Street Tower - 125 High Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/967,101
;      FILING DATE:  10-NOV-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/592,541
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-967-101-134

  Query Match             99.8%;  Score 2387;  DB 2;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
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Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
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Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
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Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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```
RESULT 8
US-08-592-541-134
; Sequence 134, Application US/08592541
; Patent No. 5986054
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  183
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  High Street Tower - 125 High Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/592,541
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-592-541-134

  Query Match             99.8%;  Score 2387;  DB 2;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 9
US-08-923-454A-10
; Sequence 10, Application US/08923454A
; Patent No. 6004794
;  GENERAL INFORMATION:
;    APPLICANT:  Creasy, Caretha
;    APPLICANT:  Livi, George
;    APPLICANT:  Karran, Eric
;    APPLICANT:  Clinkenbeard, Helen
;    APPLICANT:  Browne, Michael
;    APPLICANT:  Southan, Christopher
;    TITLE OF INVENTION:  HUMAN SERINE PROTEASE
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/923,454A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/025436
;      FILING DATE:  06-SEPT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baumeister, Kirk
;      REGISTRATION NUMBER:  33,833
;      REFERENCE/DOCKET NUMBER:  P50547
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5096
;      TELEFAX:  610-270-5090
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-923-454A-10

  Query Match             99.8%;  Score 2387;  DB 3;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 10
US-08-670-964-2
; Sequence 2, Application US/08670964
; Patent No. 6010874
;  GENERAL INFORMATION:
;    APPLICANT:  Hardy, John A.
;    TITLE OF INVENTION:  EARLY ONSET ALZHEIMER'S DISEASE
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road - UW2220; P.O. Box 15
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/670,964
;      FILING DATE:  26-JUN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/001,142
;      FILING DATE:  13-JUL-1995
;      APPLICATION NUMBER:  60/001,501
;      FILING DATE:  18-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  P50358
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-5090
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-670-964-2

  Query Match             99.8%;  Score 2387;  DB 3;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
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  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 11
US-08-888-077A-2
; Sequence 2, Application US/08888077A
; Patent No. 6020143
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE AND USES THEREFOR.
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
;      STREET:  600 SOUTH AVENUE WEST
;      CITY:  WESTFIELD
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,077A
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/592,541
;      FILING DATE:  26-JAN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PALISI, THOMAS M
;      REGISTRATION NUMBER:  36,629
;      REFERENCE/DOCKET NUMBER:  SCHERING 3.0-017 CIP CIP CIP IV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 654-5000
;      TELEFAX:  (908) 654-7866
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-888-077A-2

  Query Match             99.8%;  Score 2387;  DB 3;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 12
US-09-124-698-134
; Sequence 134, Application US/09124698
; Patent No. 6117978
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  183
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  High Street Tower - 125 High Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/124,698
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/592,541
```

```
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-124-698-134

  Query Match             99.8%;  Score 2387;  DB 3;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 13
US-09-127-480-134
; Sequence 134, Application US/09127480
; Patent No. 6194153
;  GENERAL INFORMATION:
;    APPLICANT:  ST. GEORGE-HYSLOP, PETER H
;    APPLICANT:  ROMMENS, JOHANNA M
;    APPLICANT:  FRASER, PAUL E
;    TITLE OF INVENTION:  GENETIC SEQUENCES AND PROTEINS RELATED
;    TITLE OF INVENTION:  TO ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  183
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  High Street Tower - 125 High Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/127,480
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/592,541
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-127-480-134

  Query Match             99.8%;  Score 2387;  DB 4;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 14
US-08-496-841C-134
; Sequence 134, Application US/08496841C
; Patent No. 6210919
;  GENERAL INFORMATION:
;       APPLICANT: ST. GEORGE-HYSLOP, PETER H
;                  ROMMENS, JOHANNA M
;                  FRASER, PAUL E
;       TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
;                           TO ALZHEIMER'S DISEASE
;       NUMBER OF SEQUENCES: 175
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Darby & Darby, PC
```

```
;             STREET: 805 Third Avenue
;             CITY: New York
;             STATE: New York
;             COUNTRY: U.S.A.
;             ZIP: 10022
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/496,841C
;             FILING DATE: 28-Jun-1995
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Paul F. Fehlner, Ph.D.
;             REGISTRATION NUMBER: 35,135
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 527-7700
;             TELEFAX: (212) 753-6237
;   INFORMATION FOR SEQ ID NO: 134:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 467 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-08-496-841C-134

  Query Match             99.8%;  Score 2387;  DB 4;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 15
US-08-832-867-3
; Sequence 3, Application US/08832867C
; Patent No. 6376239
; GENERAL INFORMATION:
;  APPLICANT: BAUMEISTER, Ralf
;  TITLE OF INVENTION: DNA MOLECULES COMPRISING A PROMOTER CAPABLE OF
;  TITLE OF INVENTION: CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE IN
;  TITLE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.
;  TITLE OF INVENTION: ELEGANS AND USES THEREOF
;  FILE REFERENCE: 674503-2004
;  CURRENT APPLICATION NUMBER: US/08/832,867C
;  CURRENT FILING DATE: 1997-04-04
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-08-832-867-3

  Query Match             99.8%;  Score 2387;  DB 4;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-234;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

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Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
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Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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Search completed: March 14, 2003, 20:10:18
Job time : 32 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:10:01 ; Search time 17 Seconds
(without alignments)
1266.176 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2387	99.8	467	10	US-09-754-949-4	Sequence 4, Appli
2	2387	99.8	467	10	US-09-878-454A-3	Sequence 3, Appli
3	2387	99.8	467	10	US-09-895-035-14	Sequence 14, Appl
4	2387	99.8	467	12	US-10-071-900-1	Sequence 1, Appli
5	2382	99.6	467	10	US-09-785-474-2	Sequence 2, Appli
6	2377	99.4	467	10	US-09-785-474-32	Sequence 32, Appl
7	2372	99.2	467	10	US-09-785-474-30	Sequence 30, Appl
8	2370	99.1	467	10	US-09-785-474-28	Sequence 28, Appl
9	2357	98.6	463	10	US-09-895-035-12	Sequence 12, Appl
10	2355	98.5	467	10	US-09-785-474-4	Sequence 4, Appli
11	1461	61.1	448	10	US-09-878-454A-1	Sequence 1, Appli
12	1461	61.1	448	12	US-10-071-900-2	Sequence 2, Appli
13	1453	60.8	448	10	US-09-754-949-6	Sequence 6, Appli
14	798.5	33.4	180	10	US-09-895-035-1	Sequence 1, Appli
15	659.5	27.6	354	10	US-09-823-153-8	Sequence 8, Appli
16	380	15.9	101	9	US-09-925-299-1227	Sequence 1227, Ap
17	380	15.9	101	10	US-09-925-299-1227	Sequence 1227, Ap
18	376.5	15.7	131	9	US-10-051-767-10	Sequence 10, Appl
19	366.5	15.3	129	9	US-10-051-767-11	Sequence 11, Appl
20	344	14.4	210	9	US-10-051-767-12	Sequence 12, Appl
21	308	12.9	166	9	US-10-051-767-7	Sequence 7, Appli
22	308	12.9	166	9	US-10-051-767-13	Sequence 13, Appl
23	256	10.7	74	9	US-10-051-767-9	Sequence 9, Appli
24	256	10.7	74	9	US-10-051-767-15	Sequence 15, Appl
25	243.5	10.2	65	10	US-09-864-761-38056	Sequence 38056, A
26	206	8.6	124	9	US-10-051-767-8	Sequence 8, Appli
27	206	8.6	124	9	US-10-051-767-14	Sequence 14, Appl
28	120.5	5.0	665	10	US-09-942-447-2	Sequence 2, Appli
29	112	4.7	601	10	US-09-884-430-8	Sequence 8, Appli
30	110	4.6	601	10	US-09-782-980-84	Sequence 84, Appl
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32	108	4.5	406	10	US-09-828-432-3	Sequence 3, Appli
33	108	4.5	419	10	US-09-766-693-2	Sequence 2, Appli
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36	107	4.5	831	10	US-09-789-561-86	Sequence 86, Appl
37	101.5	4.2	801	9	US-09-738-626-3760	Sequence 3760, Ap
38	99	4.1	730	9	US-09-738-626-4196	Sequence 4196, Ap
39	97	4.1	383	9	US-09-738-626-5701	Sequence 5701, Ap
40	97	4.1	764	9	US-10-045-624B-2	Sequence 2, Appli
41	97	4.1	877	10	US-09-815-242-4901	Sequence 4901, Ap
42	97	4.1	880	10	US-09-815-242-10491	Sequence 10491, A
43	94.5	4.0	737	10	US-09-899-482-2	Sequence 2, Appli
44	94	3.9	2092	9	US-10-147-026-12	Sequence 12, Appl
45	93.5	3.9	850	10	US-09-985-675-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-754-949-4
; Sequence 4, Application US/09754949
; Patent No. US20020015939A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, JUSTIN
; APPLICANT: CORDELL, BARBARA
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
; TITLE OF INVENTION: NEURONAL DEGENERATION
; FILE REFERENCE: SCIOS.012A
; CURRENT APPLICATION NUMBER: US/09/754,949
; CURRENT FILING DATE: 2001-01-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-754-949-4

Query Match 99.8%; Score 2387; DB 10; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.7e-207;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
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Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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RESULT 2
US-09-878-454A-3
; Sequence 3, Application US/09878454A
; Patent No. US20020064828A1
; GENERAL INFORMATION:
;  APPLICANT: Monteiro, et al.
;  TITLE OF INVENTION: Method  of Controlling the Binding of Calmyrin to Presenilin
;  FILE REFERENCE: 4115-161
;  CURRENT APPLICATION NUMBER: US/09/878,454A
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 60/210,939
;  PRIOR FILING DATE: 2000-06-11
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-878-454A-3

  Query Match             99.8%;  Score 2387;  DB 10;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-207;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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RESULT 3
US-09-895-035-14
; Sequence 14, Application US/09895035
; Patent No. US20020082211A1
; GENERAL INFORMATION:
;  APPLICANT: Patterson, Chandra
;  APPLICANT:  Murry, Lynn E.
;  APPLICANT:  Kaser, Matthew R.
;  TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
;  FILE REFERENCE: PC-0047 CIP
;  CURRENT APPLICATION NUMBER: US/09/895,035
;  CURRENT FILING DATE:  2001-06-29
;  PRIOR APPLICATION NUMBER: 09/116,640
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PERL Program
; SEQ ID NO 14
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020082211A1 g1709856
US-09-895-035-14

  Query Match             99.8%;  Score 2387;  DB 10;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-207;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
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Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 4
US-10-071-900-1
; Sequence 1, Application US/10071900
; Patent No. US20020127541A1
; GENERAL INFORMATION:
;  APPLICANT: St. George-Hyslop, Peter H.
;  APPLICANT:  Rommens, Johanna
;  APPLICANT:  Fraser, Paul E.
;  TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
;  TITLE OF INVENTION:  of Use
;  FILE REFERENCE: 1034/1F810-US1
;  CURRENT APPLICATION NUMBER: US/10/071,900
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;  CURRENT FILING DATE:  2002-02-08
;  PRIOR APPLICATION NUMBER: US/09/227,725
;  PRIOR FILING DATE: 1999-01-08
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-071-900-1

  Query Match             99.8%;  Score 2387;  DB 12;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-207;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
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Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
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Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 5
US-09-785-474-2
; Sequence 2, Application US/09785474
; Patent No. US20010012626A1
;   GENERAL INFORMATION:
;        APPLICANT: TANZI, RUDOLPH
;                   WASCO, WILMA
;        TITLE OF INVENTION: Genetic Alterations Related To Familial
;                            Alzheimer's Disease
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;             STREET: 1100 NEW YORK AVENUE, SUITE 600
;             CITY: WASHINGTON
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20005-3934
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/785,474
;             FILING DATE: 20-Feb-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/706,344
;             FILING DATE: 30-AUG-1996
;             APPLICATION NUMBER: 60/003,054
;             FILING DATE: 31-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: KIM, JUDITH U.
;             REGISTRATION NUMBER: 40,679
;             REFERENCE/DOCKET NUMBER: 0609.4180002
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-371-2600
;             TELEFAX: 202-371-2540
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 467 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-785-474-2

  Query Match             99.6%;  Score 2382;  DB 10;  Length 467;
  Best Local Similarity   99.6%;  Pred. No. 7.6e-207;
  Matches  465;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKHNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 6
US-09-785-474-32
; Sequence 32, Application US/09785474
; Patent No. US20010012626A1
;   GENERAL INFORMATION:
;        APPLICANT: TANZI, RUDOLPH
;                   WASCO, WILMA
;        TITLE OF INVENTION: Genetic Alterations Related To Familial
;                            Alzheimer's Disease
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;             STREET: 1100 NEW YORK AVENUE, SUITE 600
;             CITY: WASHINGTON
```

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;            STATE: DC
;            COUNTRY: USA
;            ZIP: 20005-3934
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/785,474
;            FILING DATE: 20-Feb-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/706,344
;            FILING DATE: 30-AUG-1996
;            APPLICATION NUMBER: 60/003,054
;            FILING DATE: 31-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KIM, JUDITH U.
;            REGISTRATION NUMBER: 40,679
;            REFERENCE/DOCKET NUMBER: 0609.4180002
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-371-2600
;            TELEFAX: 202-371-2540
;   INFORMATION FOR SEQ ID NO: 32:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 467 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-785-474-32

  Query Match             99.4%;  Score 2377;  DB 10;  Length 467;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-206;
  Matches  464;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLHMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKHNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 7
US-09-785-474-30
; Sequence 30, Application US/09785474
; Patent No. US20010012626A1
;   GENERAL INFORMATION:
;       APPLICANT: TANZI, RUDOLPH
;                  WASCO, WILMA
;       TITLE OF INVENTION: Genetic Alterations Related To Familial
;                           Alzheimer's Disease
;       NUMBER OF SEQUENCES: 32
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;            STREET: 1100 NEW YORK AVENUE, SUITE 600
;            CITY: WASHINGTON
;            STATE: DC
;            COUNTRY: USA
;            ZIP: 20005-3934
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/785,474
;            FILING DATE: 20-Feb-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/706,344
;            FILING DATE: 30-AUG-1996
;            APPLICATION NUMBER: 60/003,054
;            FILING DATE: 31-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KIM, JUDITH U.
;            REGISTRATION NUMBER: 40,679
;            REFERENCE/DOCKET NUMBER: 0609.4180002
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-371-2600
;            TELEFAX: 202-371-2540
;   INFORMATION FOR SEQ ID NO: 30:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 467 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-785-474-30

  Query Match             99.2%;  Score 2372;  DB 10;  Length 467;
  Best Local Similarity   99.4%;  Pred. No. 6e-206;
  Matches  464;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCLKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCLKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKHNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 8
US-09-785-474-28
; Sequence 28, Application US/09785474
; Patent No. US20010012626A1
;   GENERAL INFORMATION:
;        APPLICANT: TANZI, RUDOLPH
;                   WASCO, WILMA
;        TITLE OF INVENTION: Genetic Alterations Related To Familial
;                            Alzheimer's Disease
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;             STREET: 1100 NEW YORK AVENUE, SUITE 600
;             CITY: WASHINGTON
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20005-3934
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/785,474
;             FILING DATE: 20-Feb-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/706,344
;             FILING DATE: 30-AUG-1996
;             APPLICATION NUMBER: 60/003,054
;             FILING DATE: 31-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: KIM, JUDITH U.
;             REGISTRATION NUMBER: 40,679
;             REFERENCE/DOCKET NUMBER: 0609.4180002
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-371-2600
;             TELEFAX: 202-371-2540
;   INFORMATION FOR SEQ ID NO: 28:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 467 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-785-474-28

  Query Match             99.1%;  Score 2370;  DB 10;  Length 467;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-206;
  Matches  464;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLRPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKHNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 9
US-09-895-035-12
; Sequence 12, Application US/09895035
; Patent No. US20020082211A1
; GENERAL INFORMATION:
;  APPLICANT: Patterson, Chandra
;  APPLICANT:  Murry, Lynn E.
;  APPLICANT:  Kaser, Matthew R.
;  TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
;  FILE REFERENCE: PC-0047 CIP
;  CURRENT APPLICATION NUMBER: US/09/895,035
;  CURRENT FILING DATE:  2001-06-29
;  PRIOR APPLICATION NUMBER: 09/116,640
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PERL Program
; SEQ ID NO 12
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020082211A1 g1244638
US-09-895-035-12

  Query Match             98.6%;  Score 2357;  DB 10;  Length 463;
  Best Local Similarity   98.9%;  Pred. No. 1.3e-204;
  Matches  462;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    1;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNT----NDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 56

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     57 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 116

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    117 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 176

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    177 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 236

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    237 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 296

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    297 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 356

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    357 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 416

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    417 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 463


RESULT 10
US-09-785-474-4
; Sequence 4, Application US/09785474
; Patent No. US20010012626A1
;   GENERAL INFORMATION:
;        APPLICANT: TANZI, RUDOLPH
;                   WASCO, WILMA
;        TITLE OF INVENTION: Genetic Alterations Related To Familial
;                            Alzheimer's Disease
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;             STREET: 1100 NEW YORK AVENUE, SUITE 600
;             CITY: WASHINGTON
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20005-3934
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/785,474
;             FILING DATE: 20-Feb-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/706,344
;             FILING DATE: 30-AUG-1996
;             APPLICATION NUMBER: 60/003,054
;             FILING DATE: 31-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: KIM, JUDITH U.
;             REGISTRATION NUMBER: 40,679
;             REFERENCE/DOCKET NUMBER: 0609.4180002
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-371-2600
;             TELEFAX: 202-371-2540
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 467 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-785-474-4

  Query Match             98.5%;  Score 2355;  DB 10;  Length 467;
  Best Local Similarity   98.9%;  Pred. No. 2.1e-204;
  Matches  462;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          |||||||||||||||||||  |||| ||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLRLKGPLHMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKHNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 11
US-09-878-454A-1
; Sequence 1, Application US/09878454A
; Patent No. US20020064828A1
; GENERAL INFORMATION:
;  APPLICANT: Monteiro, et al.
;  TITLE OF INVENTION: Method  of Controlling the Binding of Calmyrin to Presenilin
;  FILE REFERENCE: 4115-161
;  CURRENT APPLICATION NUMBER: US/09/878,454A
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 60/210,939
;  PRIOR FILING DATE: 2000-06-11
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-878-454A-1

  Query Match             61.1%;  Score 1461;  DB 10;  Length 448;
  Best Local Similarity   65.5%;  Pred. No. 8.7e-124;
  Matches  305;  Conservative   39;  Mismatches   80;  Indels   42;  Gaps    8;

Qy      3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
          | | | |  :  |  ||   :   ||| :  : :|  ||    | |     ||| |
Db     24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP-----GRPPG---- 74

Qy     62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                 :|||||||||||||||||||||:||||||||| ||| |:||||||||||
Db     75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127

Qy    122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
          | :|||| |:|:||  |||||||||| |||||||||| || |||:|||:||| |::||
Db    128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy    182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
          |||| ||||||:|| |: | :|| | |||: ||||||| ||||||||||||||||||||
Db    188 LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247

Qy    242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
          |||:||:||  |||||||||||||||||||||||||| :||||||| ||| | ||:
Db    248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy    302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
          || :|  :     |: |  | :| |:  |     : | :|     : |
Db    308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------------ 349

Qy    362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
          :||       |: ||||||||||||||||||:|| |||||||:|||||||||||||
Db    350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT 402

Qy    422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||:||||||||||||:|||:|| ||:|||| || || ||
Db    403 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 448
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```
Db    403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 12
US-10-071-900-2
; Sequence 2, Application US/10071900
; Patent No. US20020127541A1
; GENERAL INFORMATION:
;  APPLICANT: St. George-Hyslop, Peter H.
;  APPLICANT:  Rommens, Johanna
;  APPLICANT:  Fraser, Paul E.
;  TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
;  TITLE OF INVENTION:  of Use
;  FILE REFERENCE: 1034/1F810-US1
;  CURRENT APPLICATION NUMBER: US/10/071,900
;  CURRENT FILING DATE:  2002-02-08
;  PRIOR APPLICATION NUMBER: US/09/227,725
;  PRIOR FILING DATE: 1999-01-08
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-071-900-2

  Query Match             61.1%;  Score 1461;  DB 12;  Length 448;
  Best Local Similarity   65.5%;  Pred. No. 8.7e-124;
  Matches  305;  Conservative   39;  Mismatches   80;  Indels   42;  Gaps    8;

Qy      3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
          | | | |  :  |  ||   :   ||| :  : :|  ||    | |     ||| |
Db     24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP-----GRPPG---- 74

Qy     62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                :|||||||||||||||||||||||:|||||||| ||| |:|||||| ||||
Db     75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTED 127

Qy    122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
          | :|||| |:|:||  |||||||||| |||||||||| || |||:|||:||| |::||
Db    128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy    182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
          |||| ||||||:|| |: | :|| | ||||: ||||||| ||||||||||||||||||||
Db    188 LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247

Qy    242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
          |||:||:||  |||||||||||||||||||||||| :|||||||| ||| | ||:
Db    248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy    302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
          || :|  :     |: |  | :| |:  |     : | :|     : |
Db    308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------------ 349

Qy    362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
          :||       |: ||||||||||||||||||:|| |||||||:||||||||||||
Db    350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT 402

Qy    422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||:|||||||||||||:|||:|| ||:|||| || || ||
Db    403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 13
US-09-754-949-6
; Sequence 6, Application US/09754949
; Patent No. US20020015939A1
; GENERAL INFORMATION:
;  APPLICANT: MCCARTHY, JUSTIN
;  APPLICANT:  CORDELL, BARBARA
;  TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
;  TITLE OF INVENTION:  NEURONAL DEGENERATION
;  FILE REFERENCE: SCIOS.012A
;  CURRENT APPLICATION NUMBER: US/09/754,949
;  CURRENT FILING DATE:  2001-01-04
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-754-949-6

  Query Match             60.8%;  Score 1453;  DB 10;  Length 448;
  Best Local Similarity   65.2%;  Pred. No. 4.6e-123;
  Matches  304;  Conservative   39;  Mismatches   81;  Indels   42;  Gaps    8;

Qy      3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
          | | | |  :  |  ||   :   ||| :  : :|  ||    | |     ||| |
Db     24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP-----GRPPG---- 74

Qy     62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                :|||||||||||||||||||||||:|||||||| ||| |:|||||| ||||
Db     75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTED 127

Qy    122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
          | :|||| |:|:||  |||||||||| |||||||||| || |||:|||:||| |::||
Db    128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy    182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
          |||| ||||||:|| |: | :|| | ||||: ||||||| ||||||||||||||||||||
Db    188 LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247

Qy    242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
          |||:||:||  |||||||||||||||||||||||| :|||||||| ||| | ||:
Db    248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy    302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
          || :|  :     |: |  | :| |:  |     : | :|     : |
Db    308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------------ 349

Qy    362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
          :||       |: ||||||||||||||||||:|| |||||||:||||||||||||
Db    350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT 402

Qy    422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||:|||||||||||||:|||:|| ||:|||| || || ||
Db    403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 14
US-09-895-035-1
; Sequence 1, Application US/09895035
; Patent No. US20020082211A1
; GENERAL INFORMATION:
;  APPLICANT: Patterson, Chandra
;  APPLICANT:  Murry, Lynn E.
;  APPLICANT:  Kaser, Matthew R.
;  TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
;  FILE REFERENCE: PC-0047 CIP
;  CURRENT APPLICATION NUMBER: US/09/895,035
;  CURRENT FILING DATE:  2001-06-29
;  PRIOR APPLICATION NUMBER: 09/116,640
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020082211A1 1353337CD1
US-09-895-035-1

  Query Match             33.4%;  Score 798.5;  DB 10;  Length 180;
```

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  Best Local Similarity   89.6%;  Pred. No. 1.4e-64;
  Matches  164;  Conservative    3;  Mismatches    7;  Indels    9;  Gaps    3;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||     ||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNT----NDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 56

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      57 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 116

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||    :   |||   |  |:
Db     117 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVS---MRHRSLLSTLF--FL 171

Qy     181 YLG 183
           :||
Db     172 WLG 174


RESULT 15
US-09-823-153-8
; Sequence 8, Application US/09823153
; Patent No. US20020025540A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  APPLICANT:  Roberts, Susan
;  APPLICANT:  Pak, Roger
;  APPLICANT:  Lewis, Martin
;  APPLICANT:  Smith, David
;  APPLICANT:  Hendrick, Joseph
;  APPLICANT:  Vinitsky, Alexander
;  TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
;  TITLE OF INVENTION:  METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
;  FILE REFERENCE: D0004
;  CURRENT APPLICATION NUMBER: US/09/823,153
;  CURRENT FILING DATE:  2001-07-02
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Description of Artificial Sequence:  PS1 PEPTIDE
US-09-823-153-8

  Query Match             27.6%;  Score 659.5;  DB 10;  Length 354;
  Best Local Similarity   75.8%;  Pred. No. 1.3e-51;
  Matches  138;  Conservative    7;  Mismatches    8;  Indels   29;  Gaps    4;

Qy     239 KYL--PEWTAWLILAVISVY---------DLVAVLCPKGPLRMLVETAQERNETLFPALI 287
           |||   :: || :   : :          |||    |:|              :||||||
Db     191 KYLKSSKYIAWPLQGWQATFGGGDHPPKSDLV----PRG--------------SLFPALI 232

Qy     288 YSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSH 347
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 YSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSH 292

Qy     348 LGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTT 407
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 LGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTT 352

Qy     408 IA 409
           ||
Db     353 IA 354


Search completed: March 14, 2003, 20:13:57
Job time : 20 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 19:20:34 ; Search time 27 Seconds
(without alignments)
1662.769 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: / 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2387	99.8	467	2	S58396	presenilin 1, spli
2	2357	98.6	463	2	S63683	presenilin I-463 -
3	2275	95.1	467	2	JC5080	presenilin 1 prote
4	2245	93.9	463	2	JC5081	presenilin 1 prote
5	2237	93.6	467	2	I78388	S182 protein - mou
6	1804	75.4	433	2	JC5390	presenilin-alpha -
7	1593	66.6	374	2	S63684	presenilin 1, spli
8	1460.5	61.1	449	2	JC5391	presenilin-beta -
9	1453	60.8	448	2	A56993	presenilin 2 - hum
10	1381.5	57.8	442	2	I39174	seven trans-membra
11	1059.5	44.3	836	2	E89453	protein F35H12.3 [
12	968.5	40.5	461	2	S60253	sel-12 protein - C
13	546.5	22.9	453	2	T00724	presenilin homolog
14	539	22.5	397	2	A84702	probable presenili
15	511	21.4	358	2	T15184	presenilin-beta ho
16	312.5	13.1	465	2	T27885	sperm membrane pro
17	125.5	5.2	2386	2	T39911	rad3 checkpoint pr
18	123.5	5.2	455	2	H97237	membrane associate
19	120.5	5.0	309	2	H90548	hypothetical prote
20	118.5	5.0	323	2	A48997	tumor surface anti
21	115.5	4.8	339	2	C71132	hypothetical prote
22	114	4.8	318	2	B84291	hypothetical prote
23	112	4.7	601	2	S12004	tyramine receptor
24	110.5	4.6	598	2	T05130	hypothetical prote
25	110	4.6	601	2	JH0170	octopamine recepto
26	109	4.6	389	2	AE1747	cell division prot
27	108.5	4.5	488	2	S46118	probable glucose t
28	108	4.5	364	2	D95959	conserved hypothet
29	107.5	4.5	887	2	S73768	MG277 homolog F11_
30	104	4.3	599	2	T24333	hypothetical prote
31	103.5	4.3	470	2	T49272	hypothetical prote
32	103.5	4.3	477	2	D84306	sodium- and chlori
33	103	4.3	578	2	D87374	RsaA secretion sys
34	102.5	4.3	682	2	T43292	G protein-linked a
35	102	4.3	398	2	B82894	conserved hypothet
36	102	4.3	547	2	T33437	hypothetical prote
37	102	4.3	707	2	T09340	hypothetical prote
38	101.5	4.2	721	2	AH3417	lpsA protein [impo
39	101.5	4.2	1492	2	A39322	cystic fibrosis tr
40	101	4.2	389	2	AD1378	cell division prot
41	101	4.2	500	2	S12899	nicotinic acetylch
42	101	4.2	651	2	T46050	hypothetical prote
43	100.5	4.2	873	2	C90594	protein-export mem
44	100.5	4.2	1148	2	H90175	NADH dehydrogenase
45	100	4.2	451	2	A96920	probable ABC trans

ALIGNMENTS

RESULT 1
S58396
presenilin 1, splice form 467 - human
N;Alternate names: Alzheimer's disease protein 3; protein S182
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999
C;Accession: S58396; S71401; S71402
R;Sherrington, R.; Rogaev, E.I.; Liang, Y.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; C
ero, I.; Pinessi, L.; Nee, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sanseau, P.; Po
E.; Rommens, J.M.; St George-Hyslop, P.H.
Nature 375, 754-760, 1995
A;Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheim
A;Reference number: I58095; MUID:95319502; PMID:7596406
A;Accession: S58396
A;Molecule type: mRNA
A;Residues: 1-467 <SHE>
A;Cross-references: EMBL:L42110; NID:g904118; PIDN:AAB46416.1; PID:g904119
R;Vidal, R.; Ghiso, J.; Wisniewski, T.; Frangione, B.
FEBS Lett. 393, 19-23, 1996
A;Title: Alzheimer's presenilin 1 gene expression in platelets and megakaryocytes. Id
A;Reference number: S71401; MUID:96397521; PMID:8804415
A;Accession: S71401
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 24-32;254-256,290-292;316-317,376-379.<VIW>
A;Experimental source: Dami megakaryotic cell line (ATCC CRL-9792) and platelets
C;Genetics:
A;Gene: GDB:PSEN1; AD3; FAD; S182; PS1
A;Cross-references: GDB:135682; OMIM:104311
A;Map position: 14q24.3-14q24.3
C;Superfamily: presenilin
C;Keywords: alternative splicing; Alzheimer's disease; glycoprotein; transmembrane pr
F;82-100/Domain: transmembrane #status predicted <TM1>
F;133-154/Domain: transmembrane #status predicted <TM2>
F;164-185/Domain: transmembrane #status predicted <TM3>
F;195-213/Domain: transmembrane #status predicted <TM4>
F;221-238/Domain: transmembrane #status predicted <TM5>
F;244-264/Domain: transmembrane #status predicted <TM6>
F;281-301/Domain: transmembrane #status predicted <TM7>
F;408-428/Domain: transmembrane #status predicted <TM8>
F;433-453/Domain: transmembrane #status predicted <TM9>
F;279,405/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.8%; Score 2387; DB 2; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-178;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 2
S63683
presenilin I-463 - human
C;Species: Homo sapiens (man)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C;Accession: S63683
R;Sahara, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, T.; M
FEBS Lett. 381, 7-11, 1996
A;Title: Identification and characterization of presenilin I-467, I-463 and I-374.
A;Reference number: S63683; MUID:96193901; PMID:8641442
A;Accession: S63683
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-463 <SAH>
A;Cross-references: EMBL:U40379; NID:g1244637; PIDN:AAB05894.1; PID:g1244638
C;Superfamily: presenilin

  Query Match             98.6%;  Score 2357;  DB 2;  Length 463;
  Best Local Similarity   98.9%;  Pred. No. 3.2e-176;
  Matches  462;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    1;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNT----NDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 56

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     57 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 116

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    117 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 176

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    177 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 236

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    237 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 296

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    297 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 356

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    357 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 416

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    417 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 463


RESULT 3
JC5080
presenilin 1 protein isoform 467 - lesser mouse lemur
C;Species: Microcebus murinus (lesser mouse lemur)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000
C;Accession: JC5080
R;Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, N.; Bell
Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A;Title: Molecular cloning, sequencing, and brain expression of the presenilin 1 gene
A;Reference number: JC5080; MUID:97079199; PMID:8920931
A;Accession: JC5080
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-467 <CAL>
A;Cross-references: EMBL:Z71333; NID:g1707591; PIDN:CAA95930.1; PID:g1707592
A;Experimental source: brain
C;Comment: This protein is an intergral membrane protein with seven transmembrane dom
C;Genetics:
A;Gene: ps1
A;Map position: 14
C;Superfamily: presenilin
C;Keywords: transmembrane protein
F;82-100/Domain: transmembrane #status predicted <TM1>
F;133-154/Domain: transmembrane #status predicted <TM2>
F;164-185/Domain: transmembrane #status predicted <TM3>
F;195-213/Domain: transmembrane #status predicted <TM4>
F;221-238/Domain: transmembrane #status predicted <TM5>
F;244-261/Domain: transmembrane #status predicted <TM6>
F;408-428/Domain: transmembrane #status predicted <TM7>

  Query Match             95.1%;  Score 2275;  DB 2;  Length 467;
  Best Local Similarity   94.9%;  Pred. No. 8e-170;
  Matches  443;  Conservative   11;  Mismatches   13;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          |||||||||||||||||||||||||||||||:|:| ||| ||:||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNREQQDHGDRRRLGNPEPLSNGRPQGNSG 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PVVERDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSVLNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||:||||: ||||:| :| |||||||||||||||| |||||||  ||||
Db    301 GDPEAQRRVSKNTKYNAQGTEREAQASVPENDDGGFSEEWEAQRDSQLGPHRSTSVSRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          |||:|||| | ||||||||||||||:|||||||||||||||||||||||||||||||||||
Db    361 VQEISSSIPASEDPEERGVKLGLGDFVFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
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Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 4
JC5081
presenilin 1 protein isoform 463 - lesser mouse lemur
C;Species: Microcebus murinus (lesser mouse lemur)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
C;Accession: JC5081
R;Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, N.; Bellis,
Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A;Title: Molecular cloning, sequencing, and brain expression of the presenilin 1 gene in
A;Reference number: JC5080; MUID:97079199; PMID:8920931
A;Contents: brain
A;Accession: JC5081
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-463 <CAL>
A;Cross-references: EMBL:Z71333
C;Comment: This protein is an intermembrane protein with seven transmembrane domains. It
C;Genetics:
A;Gene: ps1
A;Map position: 14
C;Superfamily: presenilin
C;Keywords: transmembrane protein
F;78-96/Domain: transmembrane #status predicted <TM1>
F;129-150/Domain: transmembrane #status predicted <TM2>
F;160-181/Domain: transmembrane #status predicted <TM3>
F;191-209/Domain: transmembrane #status predicted <TM4>
F;217-234/Domain: transmembrane #status predicted <TM5>
F;240-257/Domain: transmembrane #status predicted <TM6>
F;404-424/Domain: transmembrane #status predicted <TM7>

  Query Match             93.9%;  Score 2245;  DB 2;  Length 463;
  Best Local Similarity   94.0%;  Pred. No. 1.7e-167;
  Matches  439;  Conservative   11;  Mismatches   13;  Indels    4;  Gaps    1;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||    |||||:|:| ||| ||:||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNT----NDNREQQDHGDRRRLGNPEPLSNGRPQGNSG 56

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     57 PVVERDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 116

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db    117 DTETVGQRALHSVLNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 176

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    177 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 236

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    237 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 296

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||:|||| |||||:| :| |||||||||||||||| |||||||  ||||
Db    297 GDPEAQRRVSKNTKYNAQGTEREAQASVPENDDGGFSEEWEAQRDSQLGPHRSTSVSRAA 356

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          |||:|||| | ||||||||||||||:|||||||||||||||||||||||||||||||||||
Db    357 VQEISSSIPASEDPEERGVKLGLGDFVFYSVLVGKASATASGDWNTTIACFVAILIGLCL 416

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    417 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 463


RESULT 5
I78388
S182 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999
C;Accession: I78388
R;Sherrington, R.; Rogaev, E.I.; Liang, Y.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; C
ero, I.; Pinessi, L.; Nee, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sanseau, P.; Po
E.; Rommens, J.M.; St George-Hyslop, P.H.
Nature 375, 754-760, 1995
A;Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheim
A;Reference number: I58095; MUID:95319502; PMID:7596406
A;Accession: I78388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-467 <RES>
A;Cross-references: GB:L42177; NID:g904129; PIDN:AAC42094.1; PID:g904130
C;Superfamily: presenilin

  Query Match             93.6%;  Score 2237;  DB 2;  Length 467;
  Best Local Similarity   92.5%;  Pred. No. 7.4e-167;
  Matches  432;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          |||:||||||||||||||||:| |: :|||||::|||: :||: | :|||:|||||| |||
Db      1 MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQHDRQRLDNPEPISNGRPQSNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          ||||||||||||||:|||||||| |||||:||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYVTVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||| || ||| :  |||:||: : ||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVPKNPKYNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||| |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 6
JC5390
presenilin-alpha - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C;Accession: JC5390
R;Tsujimura, A.; Yasojima, K.; Hashimoto-Gotoh, T.
Biochem. Biophys. Res. Commun. 231, 392-396, 1997
A;Title: Cloning of Xenopus presenilin-alpha and -beta cDNAs and their differential e
A;Reference number: JC5390; MUID:97223465; PMID:9070286
A;Accession: JC5390
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-433 <TSU>
A;Cross-references: DDBJ:D84427; NID:g1944353; PIDN:BAA19570.1; PID:g1944354
A;Experimental source: brain
C;Comment: This protein plays a role in negative regulation of apoptotic cascades dur
C;Superfamily: presenilin
F;48-66/Domain: transmembrane #status predicted <TM1>
F;99-119/Domain: transmembrane #status predicted <TM2>
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F;130-149/Domain: transmembrane #status predicted <TM3>
F;161-178/Domain: transmembrane #status predicted <TM4>
F;187-203/Domain: transmembrane #status predicted <TM5>
F;210-227/Domain: transmembrane #status predicted <TM6>
F;374-394/Domain: transmembrane #status predicted <TM7>

  Query Match             75.4%;  Score 1804;  DB 2;  Length 433;
  Best Local Similarity   83.0%;  Pred. No. 4.1e-133;
  Matches  357;  Conservative   27;  Mismatches   44;  Indels    2;  Gaps    2;

Qy      39 NDRRSLGHPEPLSNGRPQGNSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVA 98
           ::|||  : |  |||: | :|:||:|||||||||||||||||||||||||||||||||||
Db       5 SERRSNENSESQSNGQTQSSSQQVLEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVA 64

Qy      99 TIKSVSFYTRKDGQLIYTPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRC 158
           |||||||||| ||||||||||||||:||||||:||||| ||||||:|||||||||||||||
Db      65 TIKSVSFYTRFDGQLIYTPFTEDTESVGQRALNSILNATIMISVIIVMTILLVVLYKYRC 124

Qy     159 YKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGP 218
           ||||| ||||||||||||||:||||||||||||||||||:|||||| |||||| ||||||
Db     125 YKVIHGWLIISSLLLLFFFSYIYLGEVFKTYNVAVDYITLALLIWNFGVVGMICIHWKGP 184

Qy     219 LRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQER 278
           | |||||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db     185 LLLQQAYLIMISALMALVFIKYLPEWTTWLILAVISVYDLVAVLSPKGPLRMLVETAQER 244

Qy     279 NETLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAES-TERESQDTVAENDDGGFS 337
           ||||||||||||||:|||||:|||  ::  |  : || :: |     |: | :|:|||
Db     245 NETLFPALIYSSTMIWLVNMADGDPGLKQSASTKT-YNTQAPTAHPRSDSAASDDNGGFD 303

Qy     338 EEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKAS 397
             ||  |:: :||  |||||| ||| | |:    ||||||||||||||||||||||||||
Db     304 TTWEDHRNAQIGPINSTPESRVAVQALPSNSPPSEDPEERGVKLGLGDFIFYSVLVGKAS 363

Qy     398 ATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFM 457
           ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 ATASGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFM 423

Qy     458 DQLAFHQFYI 467
           ||||||||||
Db     424 DQLAFHQFYI 433


RESULT 7
S63684
presenilin 1, splice form 374 - human
N;Alternate names: Alzheimer's disease protein 3
C;Species: Homo sapiens (man)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C;Accession: S63684
R;Sahara, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, T.; M
FEBS Lett. 381, 7-11, 1996
A;Title: Identification and characterization of presenilin I-467, I-463 and I-374.
A;Reference number: S63683; MUID:96193901; PMID:8641442
A;Accession: S63684
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-374 <SAH>
A;Cross-references: EMBL:U40380; NID:g1244639; PIDN:AAB05895.1; PID:g1244640
C;Genetics:
A;Gene: GDB:PSEN1; AD3; FAD; S182; PS1
A;Cross-references: GDB:135682; OMIM:104311
A;Map position: 14q24.3-14q24.3
C;Superfamily: presenilin

  Query Match             66.6%;  Score 1593;  DB 2;  Length 374;
  Best Local Similarity   98.4%;  Pred. No. 1e-116;
  Matches  313;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    1;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNT----NDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 56

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      57 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 116

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     117 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 176

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     177 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 236

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     237 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 296

Qy     301 GDPEAQRRVSKNSKYNAE 318
           ||||||||||||||||||
Db     297 GDPEAQRRVSKNSKYNAE 314


RESULT 8
JC5391
presenilin-beta - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C;Accession: JC5391
R;Tsujimura, A.; Yasojima, K.; Hashimoto-Gotoh, T.
Biochem. Biophys. Res. Commun. 231, 392-396, 1997
A;Title: Cloning of Xenopus presenilin-alpha and -beta cDNAs and their differential e
A;Reference number: JC5390; MUID:97223465; PMID:9070286
A;Accession: JC5391
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-449 <TSU>
A;Cross-references: DDBJ:D84428; NID:g1944355; PIDN:BAA19571.1; PID:g1944356
A;Experimental source: brain
C;Comment: This protein plays a role in negative regulation of apoptotic cascades dur
C;Superfamily: presenilin
F;91-109/Domain: transmembrane #status predicted <TM1>
F;142-162/Domain: transmembrane #status predicted <TM2>
F;173-192/Domain: transmembrane #status predicted <TM3>
F;204-221/Domain: transmembrane #status predicted <TM4>
F;230-246/Domain: transmembrane #status predicted <TM5>
F;252-279/Domain: transmembrane #status predicted <TM6>
F;390-410/Domain: transmembrane #status predicted <TM7>

  Query Match             61.1%;  Score 1460.5;  DB 2;  Length 449;
  Best Local Similarity   63.9%;  Pred. No. 2.8e-106;
  Matches  301;  Conservative   48;  Mismatches   75;  Indels   47;  Gaps    7;

Qy       2 TELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQG---- 57
           :| |   ||    | ||    |        :|||| : : :    | : ||| |
Db      21 SESPPLPSYQDGVQASEGLETSY-------HRERQPDSTQNN----EDVPNGRTSGADAY 69

Qy      58 NSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTP 117
           ||   |   | |:|||||||||:|||||||||||||||||||||||||| |||||||||
Db      70 NSETTV---ENEEEEELTLKYGARHVIMLFVPVTLCMVVVVATIKSVSFYTEKDGQLIYTP 126

Qy     118 FTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFF 177
           |:||| :||:| |:|:|| |||||:|||| ||:|||||||| || |||:|||:||| |
Db     127 FSEDTTSVGERLLNSVLNTLIMISVILVMTIFLVLLYKYRCYKFIHGWLILSSLMLLFMF 186

Qy     178 SFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVF 237
           ::||| |||||||:|:|| |: ::||| | |||| ||||||||:|||||||||||||||
Db     187 TYIYLSEVFKTYNIAMDYPTLFMVIWNFGAVGMICIHWKGPLQLQQAYLIMISALMALVF 246

Qy     238 IKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVN 297
           |||||||:||:||  ||||||:|||||||||||||||||||| :|||||||| |:| |
Db     247 IKYLPEWSAWVILGAISVYDLLAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMMWTVG 306

Qy     298 MAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPES 357
           ||:    |  |::: ::   :|   :  ||                           |
```

```
Db    307 MAD-SATADGRMNQQVQHIDRNTPEGANSTV--------------------------ED 338

Qy    358 RAAVQELSSSILAGEDP-EERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI 416
          |   :  : | |: ||| |||||||||||||||||||||:||||||||||:|||||||
Db    339 AAETRIQTQSNLSSEDPDEERGVKLGLGDFIFYSVLVGKAAATASGDWNTTLACFVAILI 398

Qy    417 GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          ||||||||||:|||||||||||||||:|||:|| :|:|||| || || ||
Db    399 GLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNIVRPFMDTLASHQMYI 449


RESULT 9
A56993
presenilin 2 - human
N;Alternate names: Alzheimer's disease protein 4
C;Species: Homo sapiens (man)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Nov-2000
C;Accession: A56993; I58098
R;Levy-Lahad, E.; Wasco, W.; Poorkaj, P.; Romano, D.M.; Oshima, J.; Pettingell, W.H.; Yu
Science 269, 973-977, 1995
A;Title: Candidate gene for the chromosome 1 familial Alzheimer's disease locus.
A;Reference number: A56993; MUID:95365816; PMID:7638622
A;Accession: A56993
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-448 <RES>
A;Cross-references: GB:L43964; NID:g951202; PIDN:AAB59557.1; PID:g951203
R;Rogaev, E.I.; Sherrington, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Liang, Y.; Chi,
.; Cohen, B.; Lannfelt, L.; Fraser, P.E.; Rommens, J.M.; St George-Hyslop, P.H.
Nature 376, 775-778, 1995
A;Title: Familial Alzheimer's disease in kindreds with missense mutations in a gene on c
A;Reference number: I58098; MUID:95379971; PMID:7651536
A;Accession: I58098
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-122,'P',124-448 <RE2>
A;Cross-references: GB:L44577; NID:g950347; PIDN:AAC42012.1; PID:g950348
C;Genetics:
A;Gene: GDB:PSEN2; AD4; STM2; PS2; E5-1
A;Cross-references: GDB:633044; OMIM:600759
A;Map position: 1q31-1q42
C;Superfamily: presenilin

  Query Match           60.8%;  Score 1453;  DB 2;  Length 448;
  Best Local Similarity 65.2%;  Pred. No. 1.1e-105;
  Matches  304;  Conservative   89;  Mismatches   81;  Indels   42;  Gaps    8;

Qy      3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
          | | | |  :  |  ||   :   ||| :  : :|  ||    | |     ||| |
Db     24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP-----GRPPG---- 74

Qy     62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                 :|||||||||||||||||||||:|||||||| ||| |:|||||| ||||
Db     75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTED 127

Qy    122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
          | :|||| |:|:||  |||||||||| |||||||||| :|||:|||:||| |::||
Db    128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy    182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
          |||| ||||||:|| |: | :|| | |||: ||||||| ||||||||||||||||||||
Db    188 LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247

Qy    242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
          |||:||:||  |||||||||||||||||||||||||||| :|||||||| ||| | ||:
Db    248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy    302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
          || :|  :     |: |  | :| |:  |     : | :|     : |
Db    308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------------ 349

Qy    362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
          :||       |: ||||||||||||||||||||:|| |||||||:||||||||||||
Db    350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT 402

Qy    422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||:|||||||||||||:|||:||  ||:|||| || || ||
Db    403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 10
I39174
seven trans-membrane domain protein AD3LP/AD5 - human
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 29-Sep-1999
C;Accession: I39174
R;Li, J.; Ma, J.; Potter, H.
Proc. Natl. Acad. Sci. U.S.A. 92, 12180-12184, 1995
A;Title: Identification and expression analysis of a potential familial Alzheimer's d
A;Reference number: I39174; MUID:96109229; PMID:8618867
A;Accession: I39174
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-442 <RES>
A;Cross-references: EMBL:U34349; NID:g1079575; PIDN:AAC50290.1; PID:g1079576
C;Superfamily: presenilin

  Query Match           57.8%;  Score 1381.5;  DB 2;  Length 442;
  Best Local Similarity 64.4%;  Pred. No. 4e-100;
  Matches  289;  Conservative   39;  Mismatches   80;  Indels   41;  Gaps    8;

Qy      3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
          | | | |  :  |  ||   :   ||| :  : :|  ||    | |     ||| |
Db     24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP-----GRPPG---- 74

Qy     62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                 :|||||||||||||||||||||:|||||||| ||| |:|||||| ||||
Db     75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127

Qy    122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
          | :|||| |:|:||  |||||||||| |||||||||| :|||:|||:||| |::||
Db    128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy    182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
          |||| ||||||:|| |: | :|| | |||: ||||||| ||||||||||||||||||||
Db    188 LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247

Qy    242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
          |||:||:||  |||||||||||||||||||||||||||| :|||||||| ||| | ||:
Db    248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy    302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
          || :|  :     |: |  | :| |:  |     : | :|     : |
Db    308 DPSSQGAL--QLPYDPEMEEDSYDSFGE---PSYPEVFEPPLTGYPG------------ 348

Qy    362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
          :||       |:  : ||||||||||||||||||:|| |||||||:||||||||||||
Db    349 EELEE-----EEESQGGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT 403

Qy    422 LLLLAIFKKALPALPISITFGLVFYFATD 450
          |||||:|||||||||||||:|||:||
Db    404 LLLLAVFKKALPALPISITFGLIFYFSTD 432


RESULT 11
E89453
protein F35H12.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: E89453
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
```

```
A;Accession: E89453
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-836 <STO>
A;Cross-references: GB:chr_X; PIDN:AAA83176.1; PID:g1109863; GSPDB:GN00028; CESP:F35H12.
A;Note: similar to M. musculus S182 protein (GB:L42177)
C;Genetics:
A;Gene: F35H12.3
A;Map position: X

  Query Match             44.3%;  Score 1059.5;  DB 2;  Length 836;
  Best Local Similarity   51.4%;  Pred. No. 1.1e-74;
  Matches  218;  Conservative   71;  Mismatches   92;  Indels   43;  Gaps    7;

Qy      64 EQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQ-LIYTPFTEDT 122
           ::||   ||  ||||| ||| ||||:||| :|| |: :::||:: :|: |:|||  :|
Db      32 QEDENVVEEAELKYGASHVIHLFVPVSLCMALVVFTMNTITFYSQNNGRHLLYTPFVRET 91

Qy     123 ETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYL 182
           ::: :: | |: || :|: |:|:||:||:| ||| ||:|| |||:|| |||| |: ||:
Db      92 DSIVEKGLMSLGNALVMLCVVVLMTVLLIVFYKYKFYKLIHGWLIVSSFLLLFLFTTIYV 151

Qy     183 GEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLP 242
            || |:::|:   : |   : | ||:||: |||||||||| ||| :|||||||||||||
Db     152 QEVLKSFDVSPSALLVLFGLGNYGVLGMMCIHWKGPLRLQQFYLITMSALMALVFIKYLP 211

Qy     243 EWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVW---LVNMA 299
           ||| | :| |||:|||||| |||||| |||||||||| :|||||||| :::   ||
Db     212 EWTVWFVLFVISVWDLVAVLTPKGPLRYLVETAQERNEPIFPALIYSSGVIYPYVLVTAV 271

Qy     300 EGDPEAQRRVSKNS----------KYNAESTER-----------ESQDTVAENDDGGFS 337
           |   : :   | :|          ::|: :|           ||  | :   : |
Db     272 ENTTDPREPTSSDSNTSTAFPGEASCSSETPKRPKVKRIPQKVQIESNTTASTTQNSGVR 331

Qy     338 EEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKAS 397
           |           |     | ||: :       : ||||||||||||||||||:||||
Db     332 VE----------RELAAERPTVQDAN---FHRHEEEERGVKLGLGDFIFYSVLLGKAS 376

Qy     398 ATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFM 457
           :    ||||||||:|||||||.||:|||:||:|||||||  ||:||| | ::: ||:
Db     377 SYF--DWNTTIACYVAILIGLCFTLVLLAVFKRALPALPISIFSGLIFYFCTRWIITPFV 434

Qy     458 DQLA 461
           |::
Db     435 TQVS 438


RESULT 12
S60253
sel-12 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Sep-1998
C;Accession: S60253
R;Levitan, D.; Greenwald, I.
Nature 377, 351-354, 1995
A;Title: Facilitation of lin-12-mediated signalling by sel-12, a Caenorhabditis elegans
A;Reference number: S60253; MUID:96032531; PMID:7566091
A;Accession: S60253
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-461 <LEV>
A;Cross-references: EMBL:U35660
C;Superfamily: presenilin

  Query Match             40.5%;  Score 968.5;  DB 2;  Length 461;
  Best Local Similarity   50.0%;  Pred. No. 7e-68;
  Matches  205;  Conservative   65;  Mismatches   97;  Indels   43;  Gaps    7;

Qy      64 EQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQ-LIYTPFTEDT 122
           ::||   ||  ||||| ||| ||||:||| :|| |: :::||:: :|: |:  ||  :|
Db      32 QEDENVVEEAELKYGASHVIHLFVPVSLCMALVVFTMNTITFYSQNNGRHLLSHPFVRET 91

Qy     123 ETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYL 182
           ::: :: | |: || :|: |:|:||:||:| ||| ||:|| |||:|| |||| |: ||:
Db      92 DSIVEKGLMSLGNALVMLCVVVLMTVLLIVFYKYKFYKLIHGWLIVSSFLLLFLFTTIYV 151

Qy     183 GEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLP 242
            || |:::|:   : |   : | ||:||: |||||||||| ||| :|||||||||||||
Db     152 QEVLKSFDVSPSALLVLFGLGNYGVLGMMCIHWKGPLRLQQFYLITMSALMALVFIKYLP 211

Qy     243 EWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVW---LVNMA 299
           ||| | :| |||:|||||| |||||| |||||||||| :|||||||| :::   ||
Db     212 EWTVWFVLFVISVWDLVAVLTPKGPLRYLVETAQERNEPIFPALIYSSGVIYPYVLVTAV 271

Qy     300 EGDPEAQRRVSKNS----------KYNAESTER-----------ESQDTVAENDDGGFS 337
           |   : :   | :|          ::|: :|           ||  | :   : |
Db     272 ENTTDPREPTSSDSNTSTAFPGEASCSSETPKRPKVKRIPQKVQIESNTTASTTQNSGVR 331

Qy     338 EEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKAS 397
           |           |     | ||: :       : ||||||||||||||||||:||||
Db     332 VE----------RELAAERPTVQDAN---FHRHEEEERGVKLGLGDFIFYSVLLGKAS 376

Qy     398 ATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYF 447
           :    ||||||||:|||||||| ||:|||:||:|||||    :    | |
Db     377 SYF--DWNTTIACYVAILIGLCFTLVLLAVFKRALPALQFPFSPDSFFTF 424


RESULT 13
T00724
presenilin homolog F22O13.19 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C;Accession: T00724
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.;
eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, April 1998
A;Description: Genomic sequence for Arabidopsis thaliana BAC F22O13.
A;Reference number: Z14200
A;Accession: T00724
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-453 <SHI>
A;Cross-references: EMBL:AC003981; NID:g3063438; PID:g3063457; GSPDB:GN00059; ATSP:F2
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: ATSP:F22O13.19
A;Map position: 1
A;Introns: 108/1
C;Superfamily: presenilin

  Query Match             22.9%;  Score 546.5;  DB 2;  Length 453;
  Best Local Similarity   33.3%;  Pred. No. 5.9e-35;
  Matches  146;  Conservative   76;  Mismatches  146;  Indels   71;  Gaps   14;

Qy      82 VIMLFVPVTLCMVVVVATIKSVSFYT----RKDGQLIYTPFTEDTETVGQRALHSILNAA 137
           :| :  ||:::|| :||    |:|  :    |   |||     |: ||  :   |: ||
Db      13 IIGVMAPVSICMFLVVLLTYSLSVTSDPQIRSAANLIYIENPSDSTTV--KLEGSLANAI 70

Qy     138 IMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYIT 197
           : : :|  :| :||:|: |     :  ::  |:  :|          : : ::: || ||
Db      71 VFVVLIAAVTFILVLLFYYNFTNFLKHYMRFSAFFVLGTMGGAIFLSIIQHFSIPVDSIT 130

Qy     198 VALLIWNLGVVGMISIHWKG-PLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY 256
             :|::|  ::| :|:   | |: |:| |::::  ::|  | | ||||| | ||  :::|
Db     131 CFILLFNFTILGTLSVFAGGIPIVLRQCYMVVMGIVVAAWFTK-LPEWTTWFILVALALY 189

Qy     257 DLVAVLCPKGPLRMLVETAQERNETLFPALIY--------------SSTMVWLVN---- 297
           |||||| | |||::||| |  |:| | ||::|                |::  ||
Db     190 DLVAVLAPGGPLKLLVELASSRDEEL-PAMVYEARPTVSSGNQRRNRGSSLRALVGGGGV 248

Qy     298 MAEGDPEAQ-----------RRVSKNSKYNAESTE--RESQDTVAENDDGGFSEE----- 339
             | | |           | | |  ||| :        | :     ||
Db     249 SDSGSVELQAVRNHDVNQLGRENSHNMDYNAIAVRDIDNVDDGIGNGSRGGLERSPLVGS 308

Qy     340 -WEAQRDSHLGPHRSTPESRAAVQELSSSILA-----GEDPEE--------------RG 378
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Db    309 PSASEHSTSVGT-RGNMEDRESVMDEEMSPLVELMGWGDNREEARGLEESDNVVDISNRG 367

Qy    379 VKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPIS 438
          :|||||||||||||||:|   |  |  |  ||::||: ||  ||:||::: :|||||||
Db    368 IKLGLGDFIFYSVLVGRA---AMYDLMTVYACYLAIISGLGCTLILLSVYNRALPALPIS 424

Qy    439 ITFGLVFYFATDYLVQPFM 457
          |  |:|||| |  |::||:
Db    425 IMLGVVFYFLTRLLMEPFV 443


RESULT 14
A84702
probable presenilin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: A84702
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84702
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <STO>
A;Cross-references: GB:AE002093; NID:g4567215; PIDN:AAD23630.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g29900
A;Map position: 2
C;Superfamily: presenilin

  Query Match             22.5%;  Score 539;  DB 2;  Length 397;
  Best Local Similarity   33.8%;  Pred. No. 1.9e-34;
  Matches  144;  Conservative   79;  Mismatches  145;  Indels   58;  Gaps   15;

Qy     52 NGRPQGNSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATI---------KS 102
          | ||    | :::   ||             :| :  ||::||  ||  :          |
Db      4 NQRP----RSILDSLGEE------------LIAILTPVSICMFTVVLLVCILNSDPSSSS 47

Qy    103 VSFYTRKDGQLIYTPFTE-DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKV 161
           ||       :    ::| |:::   : : ::||: : :: | | | :||:|:  || |
Db     48 ASF-----SSIATAAYSESDSDSSWDKFVGALLNSVVFVAAITVATFVLVLLFYLRCVKF 102

Qy    162 IHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHW-KGPLR 220
          :  ::  |: ::|       |  :   :   :| ||  :|::|  |||: ::   |  :
Db    103 LKFYMGFSAFIVLGNLGGEILVLLIDRFRFPIDSITFLILLFNFSVVGVFAVFMSKFSIL 162

Qy    221 LQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNE 280
          : | ||: |  |:|  |   |||| |::|  :::||: ||| | ||||:||| |  |:|
Db    163 ITQGYLVWIGVLVA-YFFTLLPEWTTWVLLVALALYDIAAVLLPVGPLRLLVEMAISRDE 221

Qy    281 TLFPALIYSSTMVWLVNMAEGDPEAQRRV---SKNSKYNAESTE-RESQDTVAENDDGGF 336
          : |||:| :  |    :       ||||    ::|: ||   | |  :    | :  |
Db    222 DI-PALVYEARPV----IRNDSRSVQRRVWREQRSSQNNANRNEVRVVESAEVEEEHVGS 276

Qy    337 SEEWEAQRDSHLGPHRSTP--ESRAAVQELSSSILAGEDPEERG-VKLGLGDFIFYSVLV 393
          ||  |           | |  : |    | | : | |      | :|||||||||||||
Db    277 SERAEI----------SVPLIDRRPEQAENSETFLEGIGLGSSGAIKLGLGDFIFYSVLV 326

Qy    394 GKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLV 453
          |:|   |  |  |  ||::||: || :||:|||:::::|||||||:||  |:||||    |:
Db    327 GRA---AMYDLMTVYACYLAIIAGLGITLMLLSVYQKALPALPVSIMLGVVFYFLARLLL 383

Qy    454 QPFMDQ 459
          : |: |
Db    384 EVFVVQ 389


RESULT 15
T15184
presenilin-beta homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T15184; T42237
R;Connell, M.; Maggi, L.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C18E3.
A;Reference number: Z18304
A;Accession: T15184
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-358 <CON>
A;Cross-references: EMBL:AF000265; NID:g1947147; PID:g1947155; PIDN:AAB52948.1; GSPDB
A;Experimental source: strain Bristol N2; clone C18E3
R;Li, X.; Greenwald, I.
Proc. Natl. Acad. Sci. U.S.A. 94, 12204-12209, 1997
A;Title: HOP-1, a Caenorhabditis elegans presenilin, appears to be functionally redun
A;Reference number: Z22112; MUID:98004548; PMID:9342387
A;Accession: T42237
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-358 <LIX>
A;Cross-references: EMBL:AF021905; NID:g2618986; PIDN:AAB84394.1; PID:g2618987
C;Genetics:
A;Gene: HOP-1; CESP:C18E3.8
A;Map position: 1
A;Introns: 44/2; 85/3; 215/1; 263/1; 291/3

  Query Match             21.4%;  Score 511;  DB 2;  Length 358;
  Best Local Similarity   30.8%;  Pred. No. 2.6e-32;
  Matches  118;  Conservative   78;  Mismatches  145;  Indels   42;  Gaps    7;

Qy     77 YGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPF-TEDTETVGQRALHSILN 135
          | | :  :  || :||: |   :|      ::  :::|  | : ||   |   |:
Db      8 YSGKTITGVLYPVAICMLFVAINVKLSQPEQQEQSKVVYGLFHSYDTADSGTITLY---- 63

Qy    136 AAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDY 195
             :|  ::: | | |  |: : || |  ::: :|: :|  :|  :   : :  :: |
Db     64 ---LIGFLILTTSLGVFCYQMKFYKAIKVYVLANSIGILLVYSVFHFQRIAEAQSIPVSV 120

Qy    196 ITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISV 255
           |   ||   | :|:  :|||   || | ||||:: | |:  :  ||:|| |: |  ||
Db    121 PTFFFLILQFGGLGITCLHWKSHRRLHQFYLIMLAGLTAIFILNILPDWTVWMALTAISF 180

Qy    256 YDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKY 315
          :|:|||| | |||:|||||  | :  |||::|:|:                  |  ::
Db    181 WDIVAVLTPCGPLKMLVETANRRGDDKFPAILYNSS-----------------SYVNEV 222

Qy    316 NAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPE 375
          ::  | | :   : | ::   |   |:  || | |    |     |:|:  :|
Db    223 DSPDTTRSNSTPLTEFNNSSSSRLLES--DSLLRP-PVIPRQIREVREVEGTI------- 272

Qy    376 ERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPAL 435
              :||:|||:|||:::|    |      | :||||: |:|| :|| :: : : |||||
Db    273 ----RLGMGDFVFYSLMLGNTVQTC--PLPTVVACFVSNLVGLTITLPIVTLSQTALPAL 326

Qy    436 PISITFGLVFYFATDYLVQPFMD 458
          |  :    :|||::   : || |
Db    327 PFPLAIAAIFYFSSHIALTPFTD 349


Search completed: March 14, 2003, 20:09:41
Job time : 40 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 19:19:10 ; Search time 16 Seconds
(without alignments)
1210.590 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2387	99.8	467	1	PSN1_HUMAN	P49768 homo sapien
2	2275	95.1	467	1	PSN1_MICMU	P79802 microcebus
3	2237	93.6	467	1	PSN1_MOUSE	P49769 mus musculu
4	2209.5	92.4	468	1	PSN1_RAT	P97887 rattus norv
5	2184.5	91.4	478	1	PSN1_BOVIN	Q9xt97 bos taurus
6	1804	75.4	433	1	PSN1_XENLA	O12976 xenopus lae
7	1461	61.1	448	1	PSN2_HUMAN	P49810 homo sapien
8	1460.5	61.1	449	1	PSN2_XENLA	O12977 xenopus lae
9	1449	60.6	445	1	PSN2_MICMU	P79801 microcebus
10	1441.5	60.3	449	1	PSN2_BOVIN	Q9xt96 bos taurus
11	1439	60.2	448	1	PSN2_MOUSE	Q61144 mus musculu
12	1439	60.2	448	1	PSN2_RAT	O88777 rattus norv
13	1177.5	49.2	541	1	PSN_DROME	O02194 drosophila
14	1059.5	44.3	444	1	PSN_CAEEL	P52166 caenorhabdi
15	546.5	22.9	453	1	PSNH_ARATH	O64668 arabidopsis
16	511	21.4	358	1	HOP1_CAEEL	O02100 caenorhabdi
17	312.5	13.1	465	1	SPE4_CAEEL	Q01608 caenorhabdi
18	125.5	5.2	2386	1	RAD3_SCHPO	Q02099 schizosacch
19	118.5	5.0	323	1	CD47_HUMAN	Q08722 homo sapien
20	112	4.7	601	1	OAR_DROME	P22270 drosophila
21	108.5	4.5	488	1	YB91_YEAST	P38142 saccharomyc
22	107.5	4.5	971	1	Y277_MYCPN	P75387 mycoplasma
23	105.5	4.4	436	1	A2AR_CARAU	P32251 carassius a
24	102.5	4.3	2365	1	CCAH_MOUSE	O88427 mus musculu
25	101.5	4.2	1492	1	CFTR_SQUAC	P26362 squalus aca
26	101	4.2	519	1	ACH4_DROME	P25162 drosophila
27	101	4.2	1580	1	ACC8_HUMAN	Q09428 homo sapien
28	100	4.2	441	1	DIHR_ACHDO	Q16983 acheta dome
29	99.5	4.2	970	1	Y277_MYCGE	Q49409 mycoplasma
30	99	4.1	1581	1	ACC8_RAT	Q09429 rattus norv
31	98.5	4.1	298	1	FIG1_YEAST	P38224 saccharomyc
32	98.5	4.1	385	1	CYB_ACACA	Q37378 acanthamoeb
33	97.5	4.1	354	1	C3X1_MOUSE	Q9z0d9 mus musculu
34	97	4.1	764	1	TSHR_MOUSE	P47750 mus musculu
35	97	4.1	776	1	CME3_BACSU	P39695 bacillus su
36	96.5	4.0	226	1	NU6M_DICDI	Q37314 dictyosteli
37	96.5	4.0	763	1	TSHR_BOVIN	Q27987 bos taurus
38	96	4.0	458	1	NU4M_PETMA	Q35542 petromyzon
39	95	4.0	522	1	C822_SOYBN	O81972 glycine max
40	95	4.0	628	1	YEH5_YEAST	P39980 saccharomyc
41	95	4.0	672	1	HYFB_ECOLI	P23482 escherichia
42	95	4.0	871	1	YA7D_SCHPO	Q09766 schizosacch
43	95	4.0	944	1	MML3_MYCTU	O53657 mycobacteri
44	95	4.0	1558	1	YK83_YEAST	P36028 saccharomyc
45	94	3.9	294	1	OPPC_LACLA	Q07743 lactococcus

ALIGNMENTS

RESULT 1
PSN1_HUMAN
ID PSN1_HUMAN STANDARD; PRT; 467 AA.
AC P49768; Q14762; Q15719; Q15720;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Presenilin 1 (PS-1) (S182 protein).
GN PSEN1 OR PSNL1 OR AD3 OR PS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS AD (ISOFORMS I-467 AND I-463).
RC TISSUE=Brain;
RX MEDLINE=95319502; PubMed=7596406;
RA Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Levesque G.,
RA Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar L.,
RA Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero I.,
RA Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A.,
RA Sanseau P., Polinsky R.J., Wasco W., da Silva H.A.R., Haines J.L.,
RA Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA Rommens J.M., St George-Hyslop P.H.;
RT "Cloning of a gene bearing missense mutations in early-onset familial
RT Alzheimer's disease.";
RL Nature 375:754-760(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS I-463 AND I-374).
RC TISSUE=Blood, and Brain;
RX MEDLINE=96193901; PubMed=8641442;
RA Sahara N., Yahagi Y.-I., Takagi H., Kondo T., Okochi M., Usami M.,
RA Shirasawa T., Mori H.;
RT "Identification and characterization of presenilin I-467, I-463 and
RT I-374.";
RL FEBS Lett. 381:7-11(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A.,
RA Madan A., Dickhoff R., Shaffer T., James R., Lasky S., Hood L.;
RT "Complete sequence of the gene for presenilin 1.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE OF 1-113 FROM N.A.
RA Tsujimura A., Hashimoto-Gotoh T.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX MEDLINE=96160372; PubMed=8574969;
RA Kovacs D.M., Fausett H.J., Page K.J., Kim T.-W., Moir R.D.,
RA Merriam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
RA Felsenstein K.M., Hyman B.T., Tanzi R.E., Wasco W.;
RT "Alzheimer-associated presenilins 1 and 2: neuronal expression in
RT brain and localization to intracellular membranes in mammalian
RT cells.";
RL Nat. Med. 2:224-229(1996).

RN [6]
RP PROCESSING.
RX MEDLINE=97317150; PubMed=9173929;
RA Podlisny M.B., Citron M., Amarante P., Sherrington R., Xia W.,
RA Zhang J., Diehl T., Levesque G., Fraser P., Haass C., Koo E.H.,
RA Seubert P., St George-Hyslop P., Teplow D.B., Selkoe D.J.;
RT "Presenilin proteins undergo heterogeneous endoproteolysis between
RT Thr291 and Ala299 and occur as stable N- and C-terminal fragments in
RT normal and Alzheimer brain tissue.";
RL Neurobiol. Dis. 3:325-337(1997).
RN [7]
RP FUNCTION, AND MUTAGENESIS OF MET-292.
RX MEDLINE=20014554; PubMed=10545183;
RA Steiner H., Romig H., Pesold B., Philipp U., Baader M., Citron M.,
RA Loetscher H., Jacobsen H., Haass C.;
RT "Amyloidogenic function of the Alzheimer's disease-associated
RT presenilin 1 in the absence of endoproteolysis.";
RL Biochemistry 38:14600-14605(1999).
RN [8]
RP FUNCTION.
RX MEDLINE=20062913; PubMed=10593990;
RA Ray W.J., Yao M., Mumm J., Schroeter E.H., Saftig P., Wolfe M.,
RA Selkoe D.J., Kopan R., Goate A.M.;
RT "Cell surface presenilin-1 participates in the gamma-secretase-like
RT proteolysis of Notch.";
RL J. Biol. Chem. 274:36801-36807(1999).
RN [9]
RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
RX MEDLINE=99221485; PubMed=10206644;
RA Wolfe M.S., Xia W., Ostaszewski B.L., Diehl T.S., Kimberly W.T.,
RA Selkoe D.J.;
RT "Two transmembrane aspartates in presenilin-1 required for presenilin
RT endoproteolysis and gamma-secretase activity.";
RL Nature 398:513-517(1999).
RN [10]
RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
RX MEDLINE=20359495; PubMed=10899933;
RA Berezovska O., Jack C., McLean P., Aster J.C., Hicks C., Xia W.,
RA Wolfe M.S., Kimberly W.T., Weinmaster G., Selkoe D.J., Hyman B.T.;
RT "Aspartate mutations in presenilin and gamma-secretase inhibitors both
RT impair notch1 proteolysis and nuclear translocation with relative
RT preservation of notch1 signaling.";
RL J. Neurochem. 75:583-593(2000).
RN [11]
RP FUNCTION, AND MUTAGENESIS OF LEU-286.
RX MEDLINE=20283925; PubMed=10811883;
RA Kulic L., Walter J., Multhaup G., Teplow D.B., Baumeister R.,
RA Romig H., Capell A., Steiner H., Haass C.;
RT "Separation of presenilin function in amyloid beta-peptide generation
RT and endoproteolysis of Notch.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5913-5918(2000).
RN [12]
RP FUNCTION.
RX PubMed=11226248;
RA Baki L., Marambaud P., Efthimiopoulos S., Georgakopoulos A., Wen P.,
RA Cui W., Shioi J., Koo E., Ozawa M., Friedrich V.L., Robakis N.K.;
RT "Presenilin-1 binds cytoplasmic epithelial cadherin, inhibits
RT cadherin/p120 association, and regulates stability and function of
RT the cadherin/catenin adhesion complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:2381-2386(2001).
RN [13]
RP INTERACTION WITH DELTA-2 CATENIN.
RX MEDLINE=99155075; PubMed=10037471;
RA Levesque G., Yu G., Nishimura M., Zhang D.M., Levesque L., Yu H.,
RA Xu D., Liang Y., Rogaeva E., Ikeda M., Duthie M., Murgolo N., Wang L.,
RA VanderVere P., Bayne M.L., Strader C.D., Rommens J.M., Fraser P.E.,
RA St George-Hyslop P.;
RT "Presenilins interact with armadillo proteins including
RT neural-specific plakophilin-related protein and beta-catenin.";
RL J. Neurochem. 72:999-1008(1999).
RN [14]
RP REVIEW ON VARIANTS.
RX MEDLINE=97029239; PubMed=8875251;
RA Cruts M., Hendriks L., Van Broeckhoven C.;
RT "The presenilin genes: a new gene family involved in Alzheimer disease
RT pathology.";
RL Hum. Mol. Genet. 5:1449-1455(1996).
RN [15]
RP REVIEW ON VARIANTS.
RX MEDLINE=98180715; PubMed=9521418;
RA Cruts M., van Broeckhoven C.;
RT "Presenilin mutations in Alzheimer's disease.";
RL Hum. Mutat. 11:183-190(1998).
RN [16]
RP VARIANTS AD THR-143 AND ALA-384.
RX MEDLINE=96177673; PubMed=8634711;
RA Cruts M., Backhovens H., Wang S.-Y., van Gassen G., Theuns J.,
RA de Jonghe C., Wehnert A., de Voecht J., de Winter G., Cras P.,
RA Bruyland M., Datson N., Weissenbach J., den Dunnen J.T., Martin J.-J.,
RA Hendriks L., Van Broeckhoven C.;
RT "Molecular genetic analysis of familial early-onset Alzheimer's
RT disease linked to chromosome 14q24.3.";
RL Hum. Mol. Genet. 4:2363-2372(1995).
RN [17]
RP VARIANTS AD L-82; H-115; T-139; R-163; T-231; L-264; V-392 AND Y-410.
RX MEDLINE=96177674; PubMed=8634712;
RA Campion D., Flaman J.-M., Brice A., Hannequin D., Dubois B.,
RA Martin C., Moreau V., Charbonnier F., Didierjean O., Tardieu S.,
RA Penet C., Puel M., Pasquier F., le Doze F., Bellis G., Calenda A.,
RA Heilig R., Martinez M., Mallet J., Bellis M., Clerget-Darpoux F.,
RA Agid Y., Frebourg T.;
RT "Mutations of the presenilin I gene in families with early-onset
RT Alzheimer's disease.";
RL Hum. Mol. Genet. 4:2373-2377(1995).
RN [18]
RP VARIANTS AD VAL-260; VAL-285 AND VAL-392.
RX MEDLINE=95379971; PubMed=7651536;
RA Rogaev E.I., Sherrington R., Rogaeva E.A., Levesque G., Ikeda M.,
RA Liang Y., Chi H., Lin C., Holman K., Tsuda T., Mar L., Sorbi S.,
RA Nacmias B., Piacentini S., Amaducci L., Chumakov I., Cohen D.,
RA Lannfelt L., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
RT "Familial Alzheimer's disease in kindreds with missense mutations in
RT a gene on chromosome 1 related to the Alzheimer's disease type 3
RT gene.";
RL Nature 376:775-778(1995).
RN [19]
RP VARIANTS AD V-139; V-146; Y-163; T-267; A-280 AND G-280.
RX MEDLINE=96024664; PubMed=7550356;
RA Clark R.F., Hutton M., Fuldner R.A., Froelich S., Karran E.,
RA Talbot C., Crook R., Lendon C.L., Prihar G., He C., Korenblat K.,
RA Martinez A., Wragg M., Busfield F., Behrens M.I., Myers A., Norton J.,
RA Morris J., Mehta N., Pearson C., Lincoln S., Baker M., Duff K.,
RA Zehr C., Perez-Tur J., Houlden H., Ruiz A., Ossa J., Lopera F.,
RA Arcos M., Madrigal L., Collinge J., Humphreys C., Asworth T.,
RA Sarner S., Fox N.C., Harvey R., Kennedy A., Roques P.K., Cline R.T.,
RA Phillips C.A., Venter J.C., Forsel L., Axelman K., Lilius L.,
RA Johnston J., Cowburn R., Viitanen M., Winblad B., Kosik K.S.,
RA Haltia M., Poyhonen M., Dickson D., Mann D., Neary D., Snowden J.,
RA Lantos P., Lannfelt L., Rossor M.N., Roberts G.W., Adams M.D.,
RA Hardy J., Goate A.M.;
RT "The structure of the presenilin 1 (S182) gene and identification of
RT six novel mutations in early onset AD families.";
RL Nat. Genet. 11:219-222(1995).
RN [20]
RP VARIANTS AD PHE-96; ARG-163 AND THR-213.
RX MEDLINE=96310408; PubMed=8733303;
RA Kamino K., Sato S., Sakaki Y., Yoshiiwa A., Nishiwaki Y., Takeda H.,
RA Tanabe H., Nishimura T., Li K., St George-Hyslop P.H., Miki T.,
RA Ogihara T.;
RT "Three different mutations of presenilin 1 gene in early-onset
RT Alzheimer's disease families.";
RL Neurosci. Lett. 208:195-198(1996).
RN [21]
RP VARIANT AD ASP-135.
RX MEDLINE=97369208; PubMed=9225696;
RA Crook R., Ellis R., Shanks M., Thal L.J., Perez-Tur J., Baker M.,

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  Query Match             99.8%;  Score 2387;  DB 1;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-150;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 2
PSN1_MICMU
ID   PSN1_MICMU     STANDARD;      PRT;   467 AA.
AC   P79802;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 1 (PS-1).
GN   PSEN1 OR PSNL1 OR PS1.
OS   Microcebus murinus (Lesser mouse lemur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC   Microcebus.
OX   NCBI_TaxID=30608;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97079199; PubMed=8920931;
RA   Calenda A., Mestre-Frances N., Czech C., Pradier L., Bons N.,
RA   Bellis M.;
RT   "Molecular cloning, sequencing, and brain expression of the
RT   presenilin 1 gene in Microcebus murinus.";
RL   Biochem. Biophys. Res. Commun. 228:430-439(1996).
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC       MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; I-467 (SHOWN HERE) AND I-
CC       463; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN NEURONS OF THE
CC       DIFFERENT CORTICAL LAYERS AND HIPPOCAMPUS BUT ALSO IN SUBCORTICAL
CC       STRUCTURES.
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z71333; CAA95930.1; -.
DR   MEROPS; A22.001; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack;
KW   Alternative splicing.
FT   CHAIN         1    298       PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       299    467       PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN        1     81       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     82    102       POTENTIAL.
FT   DOMAIN      103    132       LUMENAL (POTENTIAL).
FT   TRANSMEM    133    153       POTENTIAL.
FT   DOMAIN      154    160       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    161    181       POTENTIAL.
FT   DOMAIN      182    190       LUMENAL (POTENTIAL).
FT   TRANSMEM    191    211       POTENTIAL.
FT   DOMAIN      212    220       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    221    241       POTENTIAL.
FT   DOMAIN      242    243       LUMENAL (POTENTIAL).
FT   TRANSMEM    244    264       POTENTIAL.
FT   DOMAIN      265    407       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    408    428       POTENTIAL.
FT   TRANSMEM    433    453       POTENTIAL.
FT   SITE        291    292       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                SIMILARITY).
FT   SITE        292    293       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                SIMILARITY).
FT   VARSPLIC     26     29       MISSING (IN ISOFORM I-463).
SQ   SEQUENCE   467 AA;  52384 MW;  D986FF2CA7F2975C CRC64;

  Query Match             95.1%;  Score 2275;  DB 1;  Length 467;
  Best Local Similarity   94.9%;  Pred. No. 3.5e-143;
  Matches  443;  Conservative   11;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           |||||||||||||||||||||||||||||||:|:| ||| ||:||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNREQQDHGDRRRLGNPEPLSNGRPQGNSG 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 PVVERDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSVLNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||:||||: ||||:| :| |||||||||||||||| |||||||  ||||
Db     301 GDPEAQRRVSKNTKYNAQGTEREAQASVPENDDGGFSEEWEAQRDSQLGPHRSTSVSRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           |||:|||| | |||||||||||||:||||||||||||||||||||||||||||||||||||
Db     361 VQEISSSIPASEDPEERGVKLGLGDFVFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
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Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 3
PSN1_MOUSE
ID   PSN1_MOUSE     STANDARD;      PRT;   467 AA.
AC   P49769; Q9JLP9;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 1 (PS-1) (S182 protein).
GN   PSEN1 OR PSNL1 OR AD3H.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95319502; PubMed=7596406;
RA   Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Levesque G.,
RA   Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar L.,
RA   Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero I.,
RA   Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A.,
RA   Sanseau P., Polinsky R.J., Wasco W., da Silva H.A.R., Haines J.L.,
RA   Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA   Rommens J.M., St George-Hyslop P.H.;
RT   "Cloning of a gene bearing missense mutations in early-onset familial
RT   Alzheimer's disease.";
RL   Nature 375:754-760(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RX   MEDLINE=97442406; PubMed=9295283;
RA   Mitsuda N., Roses A.D., Vitek M.P.;
RT   "Transcriptional regulation of the mouse presenilin-1 gene.";
RL   J. Biol. Chem. 272:23489-23497(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SAM P8; TISSUE=Hippocampus;
RA   Kumar V.B., Vyas K.C., Choudhary V., Franko M., Flood J.F.,
RA   Morley J.E.;
RT   "Molecular cloning and tissue distribution of presenilin-1 in
RT   senenscence accelerated mice (SAM P8) mice.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC       MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L42177; AAC42094.1; -.
DR   EMBL; AF007560; AAB72049.1; -.
DR   EMBL; AF149111; AAF73153.1; -.
DR   MEROPS; A22.001; -.
DR   MGD; MGI:1202717; Psen1.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT   CHAIN         1    298       PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       299    467       PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN        1     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       POTENTIAL.
FT   DOMAIN      104    132       LUMENAL (POTENTIAL).
FT   TRANSMEM    133    153       POTENTIAL.
FT   DOMAIN      154    160       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    161    181       POTENTIAL.
FT   DOMAIN      182    194       LUMENAL (POTENTIAL).
FT   TRANSMEM    195    215       POTENTIAL.
FT   DOMAIN      216    220       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    221    241       POTENTIAL.
FT   DOMAIN      242    243       LUMENAL (POTENTIAL).
FT   TRANSMEM    244    264       POTENTIAL.
FT   DOMAIN      265    407       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    408    428       POTENTIAL.
FT   TRANSMEM    433    453       POTENTIAL.
FT   SITE        291    292       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                 SIMILARITY).
FT   SITE        292    293       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                 SIMILARITY).
FT   VARIANT       9      9       S -> T (IN STRAIN SAM P8).
FT   VARIANT      40     40       D -> E (IN STRAIN SAM P8).
FT   VARIANT      67     67       E -> CM (IN STRAIN SAM P8).
FT   VARIANT     196    196       V -> L (IN STRAIN SAM P8).
FT   VARIANT     321    322       ER -> RRD (IN STRAIN SAM P8).
SQ   SEQUENCE   467 AA;  52639 MW;  D07215B4BAD2D549 CRC64;

  Query Match             93.6%;  Score 2237;  DB 1;  Length 467;
  Best Local Similarity   92.5%;  Pred. No. 1.1e-140;
  Matches  432;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          |||:|||||||||||||||:| |: :|||||::|||: :||: | :|||:|||||| |||
Db      1 MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQHDRQRLDNPEPISNGRPQSNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||:|||||||| |||||:|||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYVTVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||| || ||| :  |||:||: : ||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVPKNPKYNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||| |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 4
PSN1_RAT
ID   PSN1_RAT       STANDARD;      PRT;   468 AA.
AC   P97887; P97529;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
```

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DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 1 (PS-1) (S182 protein).
GN   PSEN1 OR PSNL1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=97199371; PubMed=9047347;
RA   Taniguchi T., Hashimoto T., Taniguchi R., Shimada K., Kawamata T.,
RA   Yasuda M., Nakai M., Terashima A., Koizumi T., Maeda K., Tanaka C.;
RT   "Cloning of the cDNA encoding rat presenilin-1.";
RL   Gene 186:73-75(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=96255262; PubMed=8710164;
RA   Takahashi H., Murayama M., Takashima A., Mercken M., Nakazato Y.,
RA   Noguchi K., Imahori K.;
RT   "Molecular cloning and expression of the rat homologue of
RT   presenilin-1.";
RL   Neurosci. Lett. 206:113-116(1996).
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC       MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D82578; BAA11575.1; -.
DR   EMBL; D82363; BAA11564.1; -.
DR   MEROPS; A22.001; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT   CHAIN         1    298       PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       299    468       PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN        1     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       POTENTIAL.
FT   DOMAIN      104    132       LUMENAL (POTENTIAL).
FT   TRANSMEM    133    153       POTENTIAL.
FT   DOMAIN      154    160       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    161    181       POTENTIAL.
FT   DOMAIN      182    194       LUMENAL (POTENTIAL).
FT   TRANSMEM    195    215       POTENTIAL.
FT   DOMAIN      216    220       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    221    241       POTENTIAL.
FT   DOMAIN      242    243       LUMENAL (POTENTIAL).
FT   TRANSMEM    244    264       POTENTIAL.
FT   DOMAIN      265    407       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    408    428       POTENTIAL.
FT   TRANSMEM    433    453       POTENTIAL.
FT   SITE        291    292       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                 SIMILARITY).
FT   SITE        292    293       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                 SIMILARITY).
FT   CONFLICT    234    234       A -> S (IN REF. 2).
FT   CONFLICT    381    381       K -> R (IN REF. 2).
SQ   SEQUENCE   468 AA;  52790 MW;  17CB791E88A16FC0 CRC64;
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  Query Match             92.4%;  Score 2209.5;  DB 1;  Length 468;
  Best Local Similarity   92.1%;  Pred. No. 7.3e-139;
  Matches  432;  Conservative   19;  Mismatches   15;  Indels    3;  Gaps    3;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGN-S 59
           |||:|||||||||||||||:| |::|||||||:|||:|:||: | :|| :|||||| | :
Db       1 MTEIPAPLSYFQNAQMSEDSH-SSSVRSQNDNQERQQHHDRQRLDNPESISNGRPQSNFT 59

Qy      60 RQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 119
           |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 RQVIEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 119

Qy     120 EDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSF 179
           ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db     120 EDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIVSSLLLLFFFSF 179

Qy     180 IYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIK 239
           |||||||||||||||||||||||| |||||:|||||||||||||||||||||||||||||
Db     180 IYLGEVFKTYNVAVDYITVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIK 239

Qy     240 YLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMA 299
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 YLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMA 299

Qy     300 EGDPEAQRRVSKNSKYNAESTER-ESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESR 358
           |||||||||| || ||: : ||| |:|||   :||||||||||||||||||||||||||||
Db     300 EGDPEAQRRVPKNPKYSTQGTEREETQDTGTGSDDGGFSEEWEAQRDSHLGPHRSTPESR 359

Qy     359 AAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGL 418
           ||||||| |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 AAVQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGL 419

Qy     419 CLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||:|||||||||||||||||||||||||
Db     420 CLTLLLLAIFKKALPALPISITFGLIFYFATDYLVQPFMDQLAFHQFYI 468
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RESULT 5
PSN1_BOVIN
ID   PSN1_BOVIN     STANDARD;      PRT;   478 AA.
AC   Q9XT97;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 1 (PS-1).
GN   PSEN1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Sahara N., Shirasawa T., Mori H.;
RT   "Molecular cloning of bovine presenilin 1 gene.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC       FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF038936; AAD39023.1; -.
DR   MEROPS; A22.001; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT   CHAIN         1    299       PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       300    478       PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN        1     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       POTENTIAL.
FT   DOMAIN      104    133       LUMENAL (POTENTIAL).
FT   TRANSMEM    134    154       POTENTIAL.
FT   DOMAIN      155    161       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    162    182       POTENTIAL.
FT   DOMAIN      183    195       LUMENAL (POTENTIAL).
FT   TRANSMEM    196    216       POTENTIAL.
FT   DOMAIN      217    221       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    222    242       POTENTIAL.
FT   DOMAIN      243    244       LUMENAL (POTENTIAL).
FT   TRANSMEM    245    265       POTENTIAL.
FT   DOMAIN      266    418       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    419    439       POTENTIAL.
FT   TRANSMEM    444    464       POTENTIAL.
FT   SITE        292    293       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                SIMILARITY).
FT   SITE        293    294       ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT                                SIMILARITY).
SQ   SEQUENCE   478 AA;  53653 MW;  59E3FC0A1010D906 CRC64;

  Query Match             91.4%;  Score 2184.5;  DB 1;  Length 478;
  Best Local Similarity   89.5%;  Pred. No. 3.3e-137;
  Matches  428;  Conservative   19;  Mismatches   20;  Indels   11;  Gaps    2;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEH-NDRRSLGHPEPLSNGRPQGNS 59
           |||||||||||||||||||||||||||||:||| || |:||  |: | :||||   :|
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDSRERHEHGNERRRRGNTESVSNGRAPSSS 60

Qy      60 RQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 119
           :|||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QQVVEQEEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 120

Qy     120 EDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSF 179
           |||||| |||||||||| ||||||:||||||||||||||||||:||||||||||
Db     121 EDTETVAQRALHSILNAVIMISVIVIMTILLVVLYKYRCYKVIHAWLIVSSLLLLFFFSF 180

Qy     180 IYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIK 239
           |||||||||||||:|||:|||||||| |||||||:|||||||||||||||||||||||||||
Db     181 IYLGEVFKTYNVAMDYISVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIK 240

Qy     240 YLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMA 299
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 YLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMA 300

Qy     300 EGDPEAQRRVSKNSKYNAE----------STERESQDTVAENDDGGFSEEWEAQRDSHLG 349
           |||||||:||||| |||:           || |||| | |:|||||||||||||| ||
Db     301 EGDPEAQRKVSKNSNYNAQRPANSPVTTTGTESESQDPVTESDDGGFSEEWEAQRDSRLG 360

Qy     350 PHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA 409
           || || |||:|||:||||||| ||||||||||||||||||||||||||||||||||||||
Db     361 PHHSTAESRSAVQDLSSSILASEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA 420

Qy     410 CFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||:||||||:||||||||||||||||||||||||
Db     421 CFVAILIGLCLTLLLLAIFKKALPALPVSITFGLIFYFATDYLVQPFMDQLAFHQFYI 478


RESULT 6
PSN1_XENLA
ID   PSN1_XENLA     STANDARD;      PRT;   433 AA.
AC   O12976;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Presenilin alpha.
GN   PS-ALPHA.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97223465; PubMed=9070286;
RA   Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;
RT   "Cloning of Xenopus presenilin-alpha and -beta cDNAs and their
RT   differential expression in oogenesis and embryogenesis.";
RL   Biochem. Biophys. Res. Commun. 231:392-396(1997).
CC   -!- FUNCTION: MAY PLAY A ROLE IN NEGATIVE REGULATION OF APOPTOTIC
CC       CASCADES DURING OOGENESIS AND EMBRYOGENESIS, AND IN
CC       DEVELOPMENTALLY MATURED TISSUES SUCH AS BRAIN TISSUE.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN OVARIES AND TO A LESSER
CC       EXTENT IN TESTIS, INTESTINE, KIDNEY, BRAIN, EYE AND LUNG. WEAK
CC       EXPRESSION IN LIVER AND HEART. PRESENT IN TRACE AMOUNTS IN
CC       SKELETAL MUSCLE.
CC   -!- DEVELOPMENTAL STAGE: ABUNDANT IN EARLY STAGES OF OOGENESIS. THE
CC       EXPRESSION IS RAPIDLY REDUCED BETWEEN MEIOTIC MATURATION AND
CC       FERTILIZATION STAGES.
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; D84427; BAA19570.1; -.
DR   MEROPS; A22.001; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Glycoprotein.
FT   TRANSMEM     48     68       POTENTIAL.
FT   TRANSMEM     99    119       POTENTIAL.
FT   TRANSMEM    127    147       POTENTIAL.
FT   TRANSMEM    161    181       POTENTIAL.
FT   TRANSMEM    184    204       POTENTIAL.
FT   TRANSMEM    210    230       POTENTIAL.
FT   TRANSMEM    247    267       POTENTIAL.
FT   TRANSMEM    374    394       POTENTIAL.
FT   TRANSMEM    399    419       POTENTIAL.
FT   CARBOHYD    245    245       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    371    371       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   433 AA;  48301 MW;  71CCEE3F6BB9C0AF CRC64;

  Query Match             75.4%;  Score 1804;  DB 1;  Length 433;
  Best Local Similarity   83.0%;  Pred. No. 3.8e-112;
  Matches  357;  Conservative   27;  Mismatches   44;  Indels    2;  Gaps    2;

Qy      39 NDRRSLGHPEPLSNGRPQGNSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVA 98
           ::|||  : |  |||: | :|:||:||||||||||||||||||||||||||||||||||
Db       5 SERRSNENSESQSNGQTQSSSQQVLEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVA 64

Qy      99 TIKSVSFYTRKDGQLIYTPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRC 158
           |||||||||| ||||||||||||||:||||||:||||| ||||||:||||||||||||||
Db      65 TIKSVSFYTRFDGQLIYTPFTEDTESVGQRALNSILNATIMISVIIVMTILLVVLYKYRC 124

Qy     159 YKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGP 218
           ||||| ||||||||||||||:||||||||||||||||||:|||||| |||||| ||||||
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Db    125 YKVIHGWLIISSLLLLFFFSYIYLGEVFKTYNVAVDYITLALLIWNFGVVGMICIHWKGP 184

Qy    219 LRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQER 278
          | ||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db    185 LLLQQAYLIMISALMALVFIKYLPEWTTWLILAVISVYDLVAVLSPKGPLRMLVETAQER 244

Qy    279 NETLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAES-TERESQDTVAENDDGGFS 337
          |||||||||||||:||||||:|||  ::  |  : || :: |     |: | :|:|||
Db    245 NETLFPALIYSSTMIWLVNMADGDPGLKQSASTKT-YNTQAPTAHPRSDSAASDDNGGFD 303

Qy    338 EEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKAS 397
            ||  |:: :||  |||||| ||| | |:    ||||||||||||||||||||||||
Db    304 TTWEDHRNAQIGPINSTPESRVAVQALPSNSPPSEDPEERGVKLGLGDFIFYSVLVGKAS 363

Qy    398 ATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFM 457
          |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 ATASGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFM 423

Qy    458 DQLAFHQFYI 467
          ||||||||||
Db    424 DQLAFHQFYI 433


RESULT 7
PSN2_HUMAN
ID   PSN2_HUMAN     STANDARD;      PRT;   448 AA.
AC   P49810;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 2 (PS-2) (STM-2) (E5-1) (AD3LP) (AD5).
GN   PSEN2 OR PSNL2 OR AD4 OR PS2 OR STM2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT FAD ILE-141.
RX   MEDLINE=95365816; PubMed=7638622;
RA   Levy-Lahad E., Wasco W., Poorkaj P., Romano D.M., Oshima J.,
RA   Pettingell W.H., Yu C.-E., Jondro P.D., Schmidt S.D., Wang K.,
RA   Crowley A.C., Fu Y.-H., Guenette S.Y., Galas D., Nemens E.,
RA   Wijsman E.M., Bird T.D., Schellenberg G.D., Tanzi R.E.;
RT   "Candidate gene for the chromosome 1 familial Alzheimer's disease
RT   locus.";
RL   Science 269:973-977(1995).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS FAD ILE-141 AND VAL-239.
RC   TISSUE=Brain, and Colon;
RX   MEDLINE=95379971; PubMed=7651536;
RA   Rogaev E.I., Sherrington R., Rogaeva E.A., Levesque G., Ikeda M.,
RA   Liang Y., Chi H., Lin C., Holman K., Tsuda T., Mar L., Sorbi S.,
RA   Nacmias B., Piacentini S., Amaducci L., Chumakov I., Cohen D.,
RA   Lannfelt L., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
RT   "Familial Alzheimer's disease in kindreds with missense mutations in
RT   a gene on chromosome 1 related to the Alzheimer's disease type 3
RT   gene.";
RL   Nature 376:775-778(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96109229; PubMed=8618867;
RA   Li J., Ma J., Potter H.;
RT   "Identification and expression analysis of a potential familial
RT   Alzheimer disease gene on chromosome 1 related to AD3.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:12180-12184(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Levy-Lahad E., Poorkaj P., Wang K., Fu Y.H., Oshima J.,
RA   Mulligan J., Schellenberg G.D.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX   MEDLINE=96160372; PubMed=8574969;
RA   Kovacs D.M., Fausett H.J., Page K.J., Kim T.-W., Moir R.D.,
RA   Merriam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
RA   Felsenstein K.M., Hyman B.T., Tanzi R.E., Wasco W.;
RT   "Alzheimer-associated presenilins 1 and 2: neuronal expression in
RT   brain and localization to intracellular membranes in mammalian
RT   cells.";
RL   Nat. Med. 2:224-229(1996).
RN   [6]
RP   MUTAGENESIS OF ASP-366.
RX   MEDLINE=99428546; PubMed=10497236;
RA   Steiner H., Duff K., Capell A., Romig H., Grim M.G., Lincoln S.,
RA   Hardy J., Yu X., Picciano M., Fechteler K., Citron M., Kopan R.,
RA   Pesold B., Keck S., Baader M., Tomita T., Iwatsubo T., Baumeister R.,
RA   Haass C.;
RT   "A loss of function mutation of presenilin-2 interferes with amyloid
RT   beta-peptide production and notch signaling.";
RL   J. Biol. Chem. 274:28669-28673(1999).
RN   [7]
RP   MUTAGENESIS OF ASP-263 AND ASP-366.
RX   MEDLINE=20119269; PubMed=10652302;
RA   Kimberly W.T., Xia W., Rahmati T., Wolfe M.S., Selkoe D.J.;
RT   "The transmembrane aspartates in presenilin 1 and 2 are obligatory for
RT   gamma-secretase activity and amyloid beta-protein generation.";
RL   J. Biol. Chem. 275:3173-3178(2000).
RN   [8]
RP   REVIEW ON VARIANTS.
RX   MEDLINE=98180715; PubMed=9521418;
RA   Cruts M., van Broeckhoven C.;
RT   "Presenilin mutations in Alzheimer's disease.";
RL   Hum. Mutat. 11:183-190(1998).
RN   [9]
RP   VARIANT AD HIS-62.
RX   MEDLINE=98046005; PubMed=9384602;
RA   Cruts M., van Duijn C.M., Backhovens H., van den Broeck M.,
RA   Wehnert A., Serneels S., Sherrington R., Hutton M., Hardy J.,
RA   St George-Hyslop P.H., Hofman A., van Broeckhoven C.;
RT   "Estimation of the genetic contribution of presenilin-1 and -2
RT   mutations in a population-based study of presenile Alzheimer
RT   disease.";
RL   Hum. Mol. Genet. 7:43-51(1998).
RN   [10]
RP   VARIANT AD ILE-148.
RA   Lao J.I., Beyer K., Fernandez-Novoa L., Cacabelos R.;
RT   "A novel mutation in the predicted TM2 domain of the presenilin 2 gene
RT   in Spanish patient with late-onset Alzheimer's disease.";
RL   Neurogenetics 1:293-296(1998).
RN   [11]
RP   VARIANTS EOAD PRO-122 AND ILE-239.
RX   MEDLINE=20100613; PubMed=10631141;
RA   Finckh U., Mueller-Thomsen T., Mann U., Eggers C., Marksteiner J.,
RA   Meins W., Binetti G., Alberici A., Hock C., Nitsch R.M., Gal A.;
RT   "High prevalence of pathogenic mutations in patients with early-onset
RT   dementia detected by sequence analyses of four different genes.";
RL   Am. J. Hum. Genet. 66:110-117(2000).
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC       FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS. IS INVOLVED
CC       IN THE PROTEOLYTICAL PROCESSING OF AMYLOID PRECURSOR PROTEIN (APP)
CC       AND OF NOTCH1.
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT. ASSOCIATES WITH
CC       NICASTRIN AND WITH PROTEOLYTIC PROCESSED C-TERMINAL FRAGMENTS C83
CC       AND C99 OF THE AMYLOID PRECURSOR PROTEIN (APP).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM.
CC   -!- TISSUE SPECIFICITY: THE LARGER FORM IS SEEN IN THE PLACENTA,
CC       SKELETAL MUSCLE AND HEART WHILE THE SHORTER FORM IS SEEN IN THE
CC       HEART, BRAIN, PLACENTA, LIVER, SKELETAL MUSCLE AND KIDNEY.
CC   -!- PTM: HETEROGENEOUS PROTEOLYTIC PROCESSING GENERATES N-TERMINAL
CC       AND C-TERMINAL FRAGMENTS.
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES.
CC   -!- DISEASE: DEFECTS IN PSEN2 ARE RESPONSIBLE FOR EARLY-ONSET
CC       AUTOSOMAL DOMINANT ALZHEIMER DISEASE (EOAD), WHICH IS THE MOST
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CC       SEVERE FORM OF THE DISEASE, COMPLETE PENETRANCE, AN ONSET
CC       OCCURRING AS EARLY AS 30 YEARS OF AGE. THE SECOND FORM IS LATE-
CC       ONSET (LOAD) ALSO CALLED THE FAMILIAL ALZHEIMER DISEASE (FAD). AD
CC       IS A NEURODEGENERATIVE DISORDER CHARACTERIZED BY PROGRESSIVE
CC       DEMENTIA, PARKINSONISM, AND DEPOSITION OF FIBRILLAR AMYLOID
CC       PROTEINS AS INTRANEURONAL NEUROFIBRILLARY TANGLES, EXTRACELLULAR
CC       AMYLOID PLAQUES AND VASCULAR AMYLOID DEPOSITS.
CC   -!- DISEASE: THREE CAUSATIVE GENES HAVE BEEN IDENTIFIED THAT WHEN
CC       MUTATED LEAD TO PRESENILE ALZHEIMER'S DISEASE: APP (AMYLOID
CC       PRECURSOR PROTEIN GENE), PSEN1 AND PSEN2. THESE THREE GENES
CC       ACCOUNT FOR HALF OF THE FAMILIES WITH AUTOSOMAL DOMINANT PRESENILE
CC       AD, WHICH REPRESENT APPROXIMATELY 10% OF THE WHOLE AD POPULATION.
CC       IN ADDITION, APOLIPOPROTEIN E HAS BEEN IDENTIFIED AS A RISK-
CC       MODIFYING LOCUS.
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; L43964; AAB59557.1; -.
DR   EMBL; L44577; AAC42012.1; -.
DR   EMBL; U34349; AAC50290.1; -.
DR   EMBL; U50871; AAB50054.1; -.
DR   MEROPS; A22.002; -.
DR   Genew; HGNC:9509; PSEN2.
DR   MIM; 600759; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack;
KW   Alzheimer's disease; Disease mutation; Alternative splicing.
FT   CHAIN         1    297       PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       298    448       PRESENILIN 2 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN        1     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    108       POTENTIAL.
FT   DOMAIN      109    138       LUMENAL (POTENTIAL).
FT   TRANSMEM    139    159       POTENTIAL.
FT   DOMAIN      160    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    187       POTENTIAL.
FT   DOMAIN      188    200       LUMENAL (POTENTIAL).
FT   TRANSMEM    201    221       POTENTIAL.
FT   DOMAIN      222    223       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    249       LUMENAL (POTENTIAL).
FT   TRANSMEM    250    270       POTENTIAL.
FT   DOMAIN      271    388       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    389    409       POTENTIAL.
FT   TRANSMEM    414    434       POTENTIAL.
FT   VARSPLIC    263    296       MISSING (IN SHORT ISOFORM).
FT   VARIANT      62     62       R -> H (IN FAD).
FT                                /FTId=VAR_006461.
FT   VARIANT     122    122       T -> P (IN EOAD).
FT                                /FTId=VAR_009214.
FT   VARIANT     141    141       N -> I (IN FAD; VOLGA GERMAN PATIENTS).
FT                                /FTId=VAR_006462.
FT   VARIANT     148    148       V -> I (IN FAD; LOAD; SPANISH PATIENTS).
FT                                /FTId=VAR_007958.
FT   VARIANT     239    239       M -> I (IN EOAD).
FT                                /FTId=VAR_009215.
FT   VARIANT     239    239       M -> V (IN FAD; ITALIAN PATIENTS).
FT                                /FTId=VAR_006463.
FT   MUTAGEN     263    263       D->A: REDUCES PRODUCTION OF AMYLOID BETA
FT                                IN APP PROCESSING.
FT   MUTAGEN     366    366       D->A: REDUCES PRODUCTION OF AMYLOID BETA
FT                                IN APP PROCESSING AND OF NICD IN NOTCH1
FT                                PROCESSING.
FT   CONFLICT    123    123       P -> T (IN REF. 1).
FT   CONFLICT    325    325       MISSING (IN REF. 3).
FT   CONFLICT    358    358       R -> SQG (IN REF. 3).
FT   CONFLICT    432    448       NLVRPFMDTLASHQLYI -> RKHSRFIQMN (IN
FT                                REF. 3).
SQ   SEQUENCE   448 AA;  50140 MW;  A927EEC623468116 CRC64;

  Query Match             61.1%;  Score 1461;  DB 1;  Length 448;
  Best Local Similarity   65.5%;  Pred. No. 1.7e-89;
  Matches  305;  Conservative   39;  Mismatches   80;  Indels   42;  Gaps    8;

Qy       3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
           | | | |  :  |  ||   :   ||| :  : :|  ||    | |     ||| |
Db      24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP-----GRPPG---- 74

Qy      62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                  :|||||||||||||||||||||:|||||||| ||| |:||||||||||
Db      75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127

Qy     122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
           | :|||| |:|:||  |||||||||| |||||||||| || |||:|||:||| |::||
Db     128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy     182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
           |||| |||||:|| |: | :|| | |||: ||||||| ||||||||||||||||||||||
Db     188 LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247

Qy     242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
           |||:||:||  |||||||||||||||||||||||||||| :|||||||| ||| | ||:
Db     248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy     302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
           || :|  :     |: |  | :| |:  |     : | :|     : |
Db     308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------------ 349

Qy     362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
           :||       |: ||||||||||||||||||||:|| |||||||:||||||||||||
Db     350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT 402

Qy     422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||:|||||||||||||:|||:|| ||:|||| || || ||
Db     403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 8
PSN2_XENLA
ID   PSN2_XENLA     STANDARD;      PRT;   449 AA.
AC   O12977;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Presenilin beta.
GN   PS-BETA.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97223465; PubMed=9070286;
RA   Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;
RT   "Cloning of Xenopus presenilin-alpha and -beta cDNAs and their
RT   differential expression in oogenesis and embryogenesis.";
RL   Biochem. Biophys. Res. Commun. 231:392-396(1997).
CC   -!- FUNCTION: MAY PLAY A ROLE IN NEGATIVE REGULATION OF APOPTOTIC
CC       CASCADES DURING OOGENESIS AND EMBRYOGENESIS, AND IN
CC       DEVELOPMENTALLY MATURED TISSUES SUCH AS BRAIN TISSUE.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN OVARIES AND TO A LESSER
CC       EXTENT IN KIDNEY, BRAIN, EYE AND LUNG. WEAK EXPRESSION IN TESTIS,
CC       INTESTINE, LIVER AND HEART. PRESENT IN TRACE AMOUNTS IN SKELETAL
CC       MUSCLE.
CC   -!- DEVELOPMENTAL STAGE: ABUNDANT IN EARLY STAGES OF OOGENESIS AFTER
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CC       WHICH IT IS NEARLY CONSTANT.
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D84428; BAA19571.1; -.
DR   MEROPS; A22.002; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Glycoprotein.
FT   TRANSMEM     92    112       POTENTIAL.
FT   TRANSMEM    142    162       POTENTIAL.
FT   TRANSMEM    170    190       POTENTIAL.
FT   TRANSMEM    204    224       POTENTIAL.
FT   TRANSMEM    227    247       POTENTIAL.
FT   TRANSMEM    253    273       POTENTIAL.
FT   TRANSMEM    291    311       POTENTIAL.
FT   TRANSMEM    363    383       POTENTIAL.
FT   TRANSMEM    390    410       POTENTIAL.
FT   TRANSMEM    415    435       POTENTIAL.
FT   CARBOHYD    387    387       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   449 AA;  50274 MW;  2C2C105F5C723F2B CRC64;

  Query Match             61.1%;  Score 1460.5;  DB 1;  Length 449;
  Best Local Similarity   63.9%;  Pred. No. 1.8e-89;
  Matches  301;  Conservative   48;  Mismatches   75;  Indels   47;  Gaps    7;

Qy       2 TELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQG---- 57
           :| |   ||    | ||    |        :|||| : : :    | : |||  |
Db      21 SESPPLPSYQDGVQASEGLETSY-------HRERQPDSTQNN----EDVPNGRTSGADAY 69

Qy      58 NSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTP 117
           ||   |   | |:||||||||:|||||||||||||||||||||||||| |||||||||
Db      70 NSETTV---ENEEEELTLKYGARHVIMLFVPVTLCMVVVVATIKSVSFYTEKDGQLIYTP 126

Qy     118 FTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFF 177
           |:||| :||:| |:|:||  ||||||:|||| ||:|||||||| || |||:|||:||| |
Db     127 FSEDTTSVGERLLNSVLNTLIMISVILVMTIFLVLLYKYRCYKFIHGWLILSSLMLLFMF 186

Qy     178 SFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVF 237
           ::||| |||||||:|:|| |: ::||| | |||| |||||||:||||||||||||||||
Db     187 TYIYLSEVFKTYNIAMDYPTLFMVIWNFGAVGMICIHWKGPLQLQQAYLIMISALMALVF 246

Qy     238 IKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVN 297
           |||||||:||:||  ||||||:|||||||||||||||||||| :|||||||| |:| |
Db     247 IKYLPEWSAWVILGAISVYDLLAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMMWTVG 306

Qy     298 MAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPES 357
           ||:    |  |:::  ::   :|   :  ||                        |
Db     307 MAD-SATADGRMNQQVQHIDRNTPEGANSTV--------------------------ED 338

Qy     358 RAAVQELSSSILAGEDP-EERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI 416
             |  :  : | |: ||| |||||||||||||||||||||:|||||||||:||||||||
Db     339 AAETRIQTQSNLSSEDPDEERGVKLGLGDFIFYSVLVGKAAATASGDWNTTLACFVAILI 398

Qy     417 GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           ||||||||||:|||||||||||||||:|||:|| :|:|||| || || ||
Db     399 GLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNIVRPFMDTLASHQMYI 449


RESULT 9
PSN2_MICMU
ID   PSN2_MICMU     STANDARD;      PRT;   445 AA.
AC   P79801;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Presenilin 2 (PS-2) (Fragment).
GN   PSEN2 OR PSNL2 OR PS2.
OS   Microcebus murinus (Lesser mouse lemur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC   Microcebus.
OX   NCBI_TaxID=30608;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99167105; PubMed=10069575;
RA   Calenda A., Mestre-Frances N., Czech C., Pradier L., Petter A.,
RA   Perret M., Bons N., Bellis M.;
RT   "Cloning of the presenilin 2 cDNA and its distribution in brain of
RT   the primate, Microcebus murinus: coexpression with betaAPP and Tau
RT   proteins.";
RL   Neurobiol. Dis. 5:323-333(1998).
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC       FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y10140; CAA71228.1; -.
DR   MEROPS; A22.002; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT   CHAIN         1    297       PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       298    445       PRESENILIN 2 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN        1     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    108       POTENTIAL.
FT   DOMAIN      109    138       LUMENAL (POTENTIAL).
FT   TRANSMEM    139    159       POTENTIAL.
FT   DOMAIN      160    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    187       POTENTIAL.
FT   DOMAIN      188    200       LUMENAL (POTENTIAL).
FT   TRANSMEM    201    221       POTENTIAL.
FT   DOMAIN      222    223       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    249       LUMENAL (POTENTIAL).
FT   TRANSMEM    250    271       POTENTIAL.
FT   DOMAIN      272    388       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    389    409       POTENTIAL.
FT   TRANSMEM    414    434       POTENTIAL.
FT   NON_TER     445    445
SQ   SEQUENCE   445 AA;  49475 MW;  0A01A7646659E052 CRC64;

  Query Match             60.6%;  Score 1449;  DB 1;  Length 445;
  Best Local Similarity   65.2%;  Pred. No. 1e-88;
  Matches  302;  Conservative   41;  Mismatches   78;  Indels   42;  Gaps    8;

Qy       3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
           | |:| |  :  |  ||   :   | |:   : :|  ||  | | |     ||| |
Db      24 ESPSPRSCQEGGQGPEDGDSTAQWRIQDSEEDGEEDPDRYVSSGVP-----GRPPG---- 74

Qy      62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                 :|||||||||||||| |||||||:|||||||| ||| |:||||||||||
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```
Db     75 -------PEEELTLKYGAKHVIMLSVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127

Qy    122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
          | :| || |:|:||  |||||||||| |||||||||| || |||:|||:||| |::||
Db    128 TPSVSQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy    182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
          |||| ||||||:|| |: | :|| | |||: ||||||| ||||||| ||||||||||||
Db    188 LGEVLKTYNVAMDYPTLVLTVWNFGAVGMVCIHWKGPLMLQQAYLIAISALMALVFIKYL 247

Qy    242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
          |||:||:||  ||||||||||||||||||||||||||| :|||||||| ||| | ||:
Db    248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy    302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
          || :|  :     |: |  | :| |:: |     : | :||    : |
Db    308 DPSSQGAL--QLPYDPE-MEEDSYDSLGE---PSYPEVFEAPLPGYPG------------ 349

Qy    362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
          :||       |: |||||||||||||||||||:|| |||||||:||||||||||||
Db    350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT 402

Qy    422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ 464
          |||||:|||||||||||||||||:|| ||:|||| ||:||
Db    403 LLLLAVFKKALPALPISITFGLVFYFSTDNLVRPFMDTLAYHQ 445


RESULT 10
PSN2_BOVIN
ID   PSN2_BOVIN     STANDARD;      PRT;   449 AA.
AC   Q9XT96;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 2 (PS-2).
GN   PSEN2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Sahara N., Shirasawa T., Mori H.;
RT   "Molecular cloning of bovine presenilin 2 gene.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC       FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF038937; AAD39024.1; -.
DR   MEROPS; A22.002; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT   CHAIN        1    298       PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN      299    449       PRESENILIN 2 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN       1     88       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    89    109       POTENTIAL.
FT   DOMAIN     110    139       LUMENAL (POTENTIAL).
FT   TRANSMEM   140    160       POTENTIAL.
FT   DOMAIN     161    167       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   168    188       POTENTIAL.
FT   DOMAIN     189    201       LUMENAL (POTENTIAL).
FT   TRANSMEM   202    222       POTENTIAL.
FT   DOMAIN     223    224       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   225    245       POTENTIAL.
FT   DOMAIN     246    250       LUMENAL (POTENTIAL).
FT   TRANSMEM   251    271       POTENTIAL.
FT   DOMAIN     272    389       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   390    410       POTENTIAL.
FT   TRANSMEM   415    435       POTENTIAL.
SQ   SEQUENCE   449 AA;  50301 MW;  51350D05A02B2A7D CRC64;

  Query Match             60.3%;  Score 1441.5;  DB 1;  Length 449;
  Best Local Similarity   64.3%;  Pred. No. 3.3e-88;
  Matches  299;  Conservative   41;  Mismatches   86;  Indels   39;  Gaps    7;

Qy      3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSRQV 62
          | | | |     |  ||   :   |||    : :| :  | :    |   ||| |
Db     24 ESPTPRSCQDGRQGLEDGESAAQWRSQESEEDHEEEDPDRYVCSGVP---GRPPG----- 75

Qy     63 VEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDT 122
                 :|||||||||||||||||||||:||||||||| ||| |:|||||||:|||
Db     76 ------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFSEDT 129

Qy    123 ETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYL 182
           :|||| |:|:||  ||||||| ||| |||||||||| || |||:|||:||| |::|||
Db    130 PSVGQRLLNSVLNTLIMISVIVTMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYL 189

Qy    183 GEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLP 242
          ||| ||||||:|| |: | :|| | |||: ||||||| ||||||||||||||||||||
Db    190 GEVLKTYNVAMDYPTLFLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLP 249

Qy    243 EWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGD 302
          ||:||:||  |||||||||||||||||||||||||||| :|||||||| ||| | ||: |
Db    250 EWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLD 309

Qy    303 PEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQ 362
          | :|  :     |: |  | :| |:  |     : : :|     : |          :
Db    310 PSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPDVFEPPLPGYPG-----------E 351

Qy    363 ELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTL 422
          ||       |: ||||||||||||||||||:|  |||||||:|||||||||||||
Db    352 EL-------EEEEERGVKLGLGDFIFYSVLVGKAAAMGSGDWNTTLACFVAILIGLCLTL 404

Qy    423 LLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          ||||:|||||||||||||:|||:|| ||:|||| || || ||
Db    405 LLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 449


RESULT 11
PSN2_MOUSE
ID   PSN2_MOUSE     STANDARD;      PRT;   448 AA.
AC   Q61144; P97935; P97934; O54977;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 2 (PS-2) (ALG-3) (Alzheimer disease 4 homolog).
GN   PSEN2 OR PSNL2 OR ALG3 OR AD4H OR PS-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=97094860; PubMed=8940094;
RA   Vito P., Wolozin B., Ganjei J.K., Iwasaki K., Lacana E., D'Adamio L.;
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RT   "Requirement of the familial Alzheimer's disease gene PS2 for
RT   apoptosis. Opposing effect of ALG-3.";
RL   J. Biol. Chem. 271:31025-31028(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NIH Swiss;
RA   Sahara N., Mori H., Shirasawa T.;
RT   "Molecular cloning of mouse presenilin 2 gene.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 340-448 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=96152375; PubMed=8560270;
RA   Vito P., Lacana E., D'Adamio L.;
RT   "Interfering with apoptosis: Ca(2+)-binding protein ALG-2 and
RT   Alzheimer's disease gene ALG-3.";
RL   Science 271:521-525(1996).
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC       FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED, MOSTLY IN THE LIVER.
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U57324; AAC52937.1; -.
DR   EMBL; U57325; AAC53311.1; -.
DR   EMBL; AF038935; AAB92660.1; -.
DR   EMBL; U49111; AAC52935.1; -.
DR   MEROPS; A22.002; -.
DR   MGD; MGI:109284; Psen2.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT   CHAIN         1    297       PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       298    448       PRESENILIN 2 CTF SUBUNIT.
FT   DOMAIN        1     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    108       POTENTIAL.
FT   DOMAIN      109    138       LUMENAL (POTENTIAL).
FT   TRANSMEM    139    159       POTENTIAL.
FT   DOMAIN      160    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    187       POTENTIAL.
FT   DOMAIN      188    200       LUMENAL (POTENTIAL).
FT   TRANSMEM    201    221       POTENTIAL.
FT   DOMAIN      222    223       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    249       LUMENAL (POTENTIAL).
FT   TRANSMEM    250    270       POTENTIAL.
FT   DOMAIN      271    388       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    389    409       POTENTIAL.
FT   TRANSMEM    414    434       POTENTIAL.
FT   CONFLICT     87     87       R -> H (IN REF. 2).
FT   CONFLICT    226    226       A -> V (IN REF. 2).
FT   CONFLICT    324    324       MISSING (IN REF. 2).
SQ   SEQUENCE   448 AA;  49955 MW;  D6ECA9EF6360D411 CRC64;

  Query Match           60.2%;  Score 1439;  DB 1;  Length 448;
  Best Local Similarity  64.2%;  Pred. No. 4.8e-88;
  Matches  299;  Conservative   43;  Mismatches   82;  Indels   42;  Gaps    8;

Qy       3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSL-GHPEPLSNGRPQGNSRQ 61
Db      24 ESPTSRSCQEGRPGPEDGESTAQWRTQESEEDCEEDPDRYACSGAP-----GRPSG---- 74

Qy      62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
Db      75 -------LEEELTLKYGAKRVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127

Qy     122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
Db     128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy     182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
Db     188 LGEVLKTYNVAMDYPTLFLAVWNFGAVGMVCIHWKGPLALQQAYLIVISALMALVFIKYL 247

Qy     242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
Db     248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy     302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
Db     308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEAFEAPLPGYPG------------ 349

Qy     362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
Db     350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGNGDWNTTLACFIAILIGLCLT 402

Qy     422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
Db     403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 12
PSN2_RAT
ID   PSN2_RAT       STANDARD;      PRT;   448 AA.
AC   O88777; O35546; O08947;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin 2 (PS-2).
GN   PSEN2 OR PSNL2 OR PS2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RA   Frentzel S., Abdel A.S., Luebbert H.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=97473536; PubMed=9332390;
RA   Takahashi H., Mercken M., Nakazato Y., Noguchi K., Murayama M.,
RA   Imahori K., Takashima A.;
RT   "Cloning of cDNA and expression of the gene encoding rat
RT   presenilin-2.";
RL   Gene 197:383-387(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=98207716; PubMed=9545577;
RA   Tanahashi H., Tabira T.;
RT   "Cloning of the cDNA encoding rat presenilin-2.";
RL   Biochim. Biophys. Acta 1396:259-262(1998).
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC       EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC       FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC       C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
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CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X99267; CAA67663.1; -.
DR   EMBL; D83700; BAA22832.1; -.
DR   EMBL; AB004454; BAA20406.1; -.
DR   MEROPS; A22.002; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT   CHAIN         1    297       PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
FT   CHAIN       298    448       PRESENILIN 2 CTF SUBUNIT (BY SIMILARITY).
FT   DOMAIN        1     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    106       POTENTIAL.
FT   DOMAIN      107    141       LUMENAL (POTENTIAL).
FT   TRANSMEM    142    159       POTENTIAL.
FT   DOMAIN      160    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       POTENTIAL.
FT   DOMAIN      189    202       LUMENAL (POTENTIAL).
FT   TRANSMEM    203    219       POTENTIAL.
FT   DOMAIN      220    229       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    230    246       POTENTIAL.
FT   DOMAIN      247    252       LUMENAL (POTENTIAL).
FT   TRANSMEM    253    269       POTENTIAL.
FT   DOMAIN      270    386       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    387    406       POTENTIAL.
FT   TRANSMEM    414    434       POTENTIAL.
FT   CONFLICT      7      7       S -> T (IN REF. 1).
FT   CONFLICT     86     87       KH -> ND (IN REF. 3).
SQ   SEQUENCE   448 AA;  50051 MW;  299A7C416405046C CRC64;

  Query Match             60.2%;  Score 1439;  DB 1;  Length 448;
  Best Local Similarity   63.9%;  Pred. No. 4.8e-88;
  Matches  298;  Conservative   44;  Mismatches   82;  Indels   42;  Gaps    7;

Qy       3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSL-GHPEPLSNGRPQGNSRQ 61
Db      24 ESPTSRSCQDSRPGPEDGENTAQWRSQENEDDCEEDPDHYACSGVP-----GRPSG---- 74

Qy      62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
Db      75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127

Qy     122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
Db     128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy     182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
Db     188 LGEVFKTYNVAMDYPTLFLAVWNFGAVGMVCIHWKGPLVLQQAYLIVISALMALVFIKYL 247

Qy     242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
Db     248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy     302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
Db     308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEAFEAPQPGYPGEE---------- 351

Qy     362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
Db     352 ---------PEEEEERGVKLGLGDFIFYSVLVGKAAATGNGDWSTTLACFIAILIGLCLT 402

Qy     422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
Db     403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 13
PSN_DROME
ID   PSN_DROME      STANDARD;      PRT;   541 AA.
AC   O02194; O02395; O76802; Q9V3L9; Q9TY80; Q9V3S1; O96340;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Presenilin homolog (DPS) (DMPS).
GN   PSN OR PS OR CG18803/CG5868.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND DEVELOPMENTAL STAGE.
RC   TISSUE=Embryo;
RX   MEDLINE=97285868; PubMed=9141085;
RA   Boulianne G.L., Livne-Bar I., Humphreys J.M., Liang Y., Lin C.,
RA   Rogaev E., St George-Hyslop P.H.;
RT   "Cloning and characterization of the Drosophila presenilin
RT   homologue.";
RL   NeuroReport 8:1025-1029(1997).
RN   [2]
RP   SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE (SHORT ISOFORM).
RC   STRAIN=Canton-S; TISSUE=Embryo, and Head;
RX   MEDLINE=97260623; PubMed=9106743;
RA   Hong C.-S., Koo E.H.;
RT   "Isolation and characterization of Drosophila presenilin homolog.";
RL   NeuroReport 8:665-668(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), TISSUE SPECIFICITY,
RP   DEVELOPMENTAL STAGE, SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
RX   MEDLINE=99279250; PubMed=10349633;
RA   Ye Y., Fortini M.E.;
RT   "Characterization of Drosophila Presenilin and its colocalization with
RT   Notch during development.";
RL   Mech. Dev. 79:199-211(1998).
RN   [4]
RP   SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RX   MEDLINE=99221488; PubMed=10206647;
RA   Ye Y., Lukinova N., Fortini M.E.;
RT   "Neurogenic phenotypes and altered Notch processing in Drosophila
RT   Presenilin mutants.";
RL   Nature 398:525-529(1999).
RN   [5]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND DEVELOPMENTAL STAGE.
RC   STRAIN=Canton-S;
RX   MEDLINE=98331525; PubMed=9666900;
RA   Marfany G., Del-Favero J., Valero R., De Jonghe C., Woodrow S.,
RA   Hendriks L., Van Broeckhoven C., Gonzalez-Duarte R.;
RT   "Identification of a Drosophila presenilin homologue: evidence of
RT   alternatively spliced forms.";
RL   J. Neurogenet. 12:41-54(1998).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99423881; PubMed=10493744;
RA   Guo Y., Livne-Bar I., Zhou L., Boulianne G.L.;
RT   "Drosophila presenilin is required for neuronal differentiation and
RT   affects notch subcellular localization and signaling.";
RL   J. Neurosci. 19:8435-8442(1999).
RN   [7]
RP   SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE PATTERNING OF THE
CC       OPTIC LOBES. PROTEIN MAY ACT, TOGETHER WITH NOTCH, TO SPECIFY
CC       CELL FATES THROUGHOUT DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC       ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM/PS-D; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: MATERNALLY EXPRESSED IN NURSE AND FOLLICLE
CC       CELLS. IN EARLY EMBRYOS, EXPRESSED IN ALL OR MOST CELLS AND LATER
CC       INCREASES IN CNS AND EPIDERMAL TISSUES. IN LARVAE, EXPRESSION IS
CC       SEEN IN ALL IMAGINAL DISKS, BRAIN AND OPTIC LOBES. IN PUPAE,
CC       EXPRESSION IS SEEN IN EYE DISK AND BRAIN.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
CC       THROUGHOUT DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; U77934; AAB61139.1; -.
DR   EMBL; U78084; AAB53369.1; -.
DR   EMBL; AF084184; AAC33129.1; -.
DR   EMBL; AF084184; AAC33128.1; -.
DR   EMBL; AF017024; AAD01610.1; -.
DR   EMBL; AF017025; AAD01611.1; -.
DR   EMBL; AF017026; AAD01612.1; -.
DR   EMBL; AF093402; AAD52707.1; -.
DR   EMBL; AF093402; AAD52708.1; -.
DR   EMBL; AE003591; -; NOT_ANNOTATED_CDS.
DR   EMBL; AE003591; AAF51598.1; -.
DR   MEROPS; A22.UPW; -.
DR   FlyBase; FBgn0019947; Psn.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane; Glycoprotein; Alternative splicing.
FT   TRANSMEM     107     127       POTENTIAL.
FT   TRANSMEM     155     175       POTENTIAL.
FT   TRANSMEM     183     203       POTENTIAL.
FT   TRANSMEM     217     237       POTENTIAL.
FT   TRANSMEM     243     263       POTENTIAL.
FT   TRANSMEM     266     286       POTENTIAL.
FT   TRANSMEM     304     324       POTENTIAL.
FT   TRANSMEM     482     502       POTENTIAL.
FT   TRANSMEM     507     527       POTENTIAL.
FT   CARBOHYD     129     129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     339     339       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     410     410       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     384     397       MISSING (IN SHORT ISOFORM).
FT   CONFLICT      80      81       GG -> RS (IN REF. 2).
SQ   SEQUENCE   541 AA;  59304 MW;  A3B3D54348A2C03F CRC64;

  Query Match             49.2%;  Score 1177.5;  DB 1;  Length 541;
  Best Local Similarity   47.5%;  Pred. No. 1.1e-70;
  Matches  251;  Conservative   73;  Mismatches  125;  Indels   79;  Gaps    9;

Qy      17 SED-----NHLSNTVRSQNDNRERQEHNDRRSLGHPEPLS-------------NGRPQ- 56
           |||     : :    | :   | :|: |:  |    :| :               ||
Db      16 SEDDANVGSQIGAAERLERPPRRQQQRNNYGSSNQDQPDAAILAVPNVVMREPCGSRPSR 75

Qy      57 ---GNSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQL 113
              |         | :||  |||||:||| |||||:|||:|||||| |:|||   |  |
Db      76 LTGGGGGSGGPPTNEMEEEQGLKYGAQHVIKLFVPVSLCMLVVVATINSISFYNSTDVYL 135

Qy     114 IYTPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLL 173
           :|||| | :     :   :: |: |::||:|||| ||:|||| |||::|| |||:|| :|
Db     136 LYTPFHEQSPEPSVKFWSALANSLILMSVVVVMTFLLIVLYKKRCYRIIHGWLILSSFML 195

Qy     174 LFFFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALM 233
           || |:::|| |: : ||: :|| |  |::|| ||||:|||||:|||||| ||| ::|||
Db     196 LFIFTYLYLEELLRAYNIPMDYPTALLIMWNFGVVGMMSIHWQGPLRLQQGYLIFVAALM 255

Qy     234 ALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMV 293
           |||||||||||||| :|| ||::||:||| |:||||:|||||||||| :|||||||||:|
Db     256 ALVFIKYLPEWTAWAVLAAISIWDLIAVLSPRGPLRILVETAQERNEQIFPALIYSSTVV 315

Qy     294 W-LVNMAEGDPEAQRRVSKNSKYNAESTERESQDTVA--------------------END 332
           : |||              |  |  |: :| | :|:::|                   : |
Db     316 YALVNTVTPQQSQATASSSPSSSNSTTTTRATQNSLASPEAAAAASGQRTGNSHPRQNQRD 375

Qy     333 DG-----------------------GFSEEWEAQRDSHLGPH----RSTPESRAAVQEL 364
           ||                        ||::|| |     :       :||    |
Db     376 DGSVLATEGMPLVTFKSNLRGNAEAAGFTQEWSANLSERVARRQIEVQSTQSGNAQRSNE 435

Qy     365 SSSILAGED-----PEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLC 419
             :: | :       ||||:||||||||||||||||||  : ||| ||||||||||||||
Db     436 YRTVTAPDQNHPDGQEERGIKLGLGDFIFYSVLVGKAS--SYGDWTTTIACFVAILIGLC 493

Qy     420 LTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           ||||||||::|||||||||||||:| |||  :|:|||: |:  | :|
Db     494 LTLLLLAIWRKALPALPISITFGLIFCFATSAVVKPFMEDLSAKQVFI 541


RESULT 14
PSN_CAEEL
ID   PSN_CAEEL      STANDARD;      PRT;   444 AA.
AC   P52166; Q20076; Q9U9C7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Presenilin sel-12.
GN   SEL-12 OR F35H12.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
```

```
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT SER-60.
RC   STRAIN=Bristol N2;
RX   MEDLINE=96032531; PubMed=7566091;
RA   Levitan D., Greenwald I.;
RT   "Facilitation of lin-12-mediated signalling by sel-12, a
RT   Caenorhabditis elegans S182 Alzheimer's disease gene.";
RL   Nature 377:351-354(1995).
RN   [2]
RP   REVISIONS TO 84-85.
RA   Levitan D.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   STRAIN=Bristol N2;
RX   MEDLINE=20372200; PubMed=10917532;
RA   Wittenburg N., Eimer S., Lakowski B., Roehrig S., Rudolph C.,
RA   Baumeister R.;
RT   "Presenilin is required for proper morphology and function of neurons
RT   in C. elegans.";
RL   Nature 406:306-309(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Nelson J., Gattung S.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   REVISIONS.
RA   Waterston R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY FACILITATE LIN-12 MEDIATED RECEPTION OF
CC       INTERCELLULAR SIGNALS. IT MIGHT BE DIRECTLY INVOLVED IN LIN-12
CC       MEDIATED RECEPTION, FUNCTIONING AS A CO-RECEPTOR OR AS A
CC       DOWNSTREAM EFFECTOR THAT IS ACTIVATED UPON LIN-12 ACTIVATION.
CC       ALTERNATIVELY IT MAY BE INVOLVED IN A MORE GENERAL CELLULAR
CC       PROCESS SUCH AS RECEPTOR LOCALIZATION OR RECYCLING AND HENCE
CC       INFLUENCE LIN-12 ACTIVITY INDIRECTLY. Required cell-autonomously
CC       for correct neurite connectivity of the AIY cholinergic
CC       interneurones and their correct functioning in thermotaxis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in most neurons.
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U35660; AAA85511.1; -.
DR   EMBL; AF171064; AAD50991.1; -.
DR   EMBL; U41540; AAK39230.1; -.
DR   MEROPS; A22.UPW; -.
DR   WormPep; F35H12.3; CE24946.
DR   InterPro; IPR001686; Nema_presenilin.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
DR   PRINTS; PR01075; PRESENILNSEL.
KW   Transmembrane.
FT   TRANSMEM     46     66       POTENTIAL.
FT   TRANSMEM    102    122       POTENTIAL.
FT   TRANSMEM    131    151       POTENTIAL.
FT   TRANSMEM    164    184       POTENTIAL.
FT   TRANSMEM    190    210       POTENTIAL.
FT   TRANSMEM    213    233       POTENTIAL.
FT   TRANSMEM    251    271       POTENTIAL.
FT   TRANSMEM    385    405       POTENTIAL.
FT   VARIANT      60     60       C -> S (IN AR131; EGG-LAYING-DEFECTIVE).
FT   CONFLICT    413    444       PISIFSGLIFYFCTRWIITPFVTQVSQKCLLY -> QFPFS
FT                                PDSFFTFVPAGSSPHLLHKSLKSVYYINSLFLPFLCIINFS
FT                                IIS (IN REF. 1).
SQ   SEQUENCE   444 AA;  50034 MW;  37ADBC124E16429C CRC64;

  Query Match             44.3%;  Score 1059.5;  DB 1;  Length 444;
  Best Local Similarity   51.4%;  Pred. No. 5.2e-63;
  Matches  218;  Conservative   71;  Mismatches   92;  Indels   43;  Gaps    7;

Qy      64 EQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQ-LIYTPFTEDT 122
           ::|| || ||||| ||| |||||:||| :|| |: :::||:: :|: |:|||| :|
Db      32 QEDENVVEEAELKYGASHVIHLFVPVSLCMALVVFTMNTITFYSQNNGRHLLYTPFVRET 91

Qy     123 ETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYL 182
           ::: :: | |: || :|: |:|:||:||:| ||| ||:|| |||:|| |||| |: ||:
Db      92 DSIVEKGLMSLGNALVMLCVVVLMTVLLIVFYKYKFYKLIHGWLIVSSFLLLFLFTTIYV 151

Qy     183 GEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLP 242
           || |:::|:   : |   : | ||:||: |||||||||| ||| :||||||||||||
Db     152 QEVLKSFDVSPSALLVLFGLGNYGVLGMMCIHWKGPLRLQQFYLITMSALMALVFIKYLP 211

Qy     243 EWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVW---LVNMA 299
           ||| | :| ||||:|||||| |||||| |||||||||| :|||||||| :::   ||
Db     212 EWTVWFVLFVISVWDLVAVLTPKGPLRYLVETAQERNEPIFPALIYSSGVIYPYVLVTAV 271

Qy     300 EGDPEAQRRVSKNS----------KYNAESTER-----------ESQDTVAENDDGGFS 337
           |   : :   | :|           ::|: :|             ||  | :   : |
Db     272 ENTTDPREPTSSDSNTSTAFPGEASCSSETPKRPKVKRIPQKVQIESNTTASTTQNSGVR 331

Qy     338 EEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKAS 397
           |           |     | ||: :       : |||||||||||||||||:|||
Db     332 VE----------RELAAERPTVQDAN---FHRHEEEERGVKLGLGDFIFYSVLLGKAS 376

Qy     398 ATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFM 457
           :    ||||||||:|||||||| ||:|||:||:|||||||  ||:||| | ::: ||:
Db     377 SYF--DWNTTIACYVAILIGLCFTLVLLAVFKRALPALPISIFSGLIFYFCTRWIITPFV 434

Qy     458 DQLA 461
           |::
Db     435 TQVS 438


RESULT 15
PSNH_ARATH
ID   PSNH_ARATH     STANDARD;      PRT;   453 AA.
AC   O64668;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Presenilin homolog.
GN   AT1G08700 OR F22O13.18.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
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RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC003981; AAF99776.1; -.
DR   MEROPS; A22.UPW; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
KW   Transmembrane.
FT   TRANSMEM     10     30       POTENTIAL.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM    104    124       POTENTIAL.
FT   TRANSMEM    133    153       POTENTIAL.
FT   TRANSMEM    160    180       POTENTIAL.
FT   TRANSMEM    181    201       POTENTIAL.
FT   TRANSMEM    370    390       POTENTIAL.
FT   TRANSMEM    393    413       POTENTIAL.
FT   TRANSMEM    418    438       POTENTIAL.
SQ   SEQUENCE   453 AA;  49308 MW;  7FBDD9B86D97955E CRC64;

  Query Match             22.9%;  Score 546.5;  DB 1;  Length 453;
  Best Local Similarity   33.3%;  Pred. No. 3.7e-29;
  Matches  146;  Conservative   76;  Mismatches  146;  Indels   71;  Gaps   14;

Qy      82 VIMLFVPVTLCMVVVVATIKSVSFYT----RKDGQLIYTPFTEDTETVGQRALHSILNAA 137
           :| :  ||::|| :||    |:|  :    |   |||     |: ||  :   |: ||
Db      13 IIGVMAPVSICMFLVVLLTYSLSVTSDPQIRSAANLIYIENPSDSTTV--KLEGSLANAI 70

Qy     138 IMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYIT 197
           : : :|  :| :||:|: |     :  ::  |:  :|          : : ::: || ||
Db      71 VFVVLIAAVTFILVLLFYYNFTNFLKHYMRFSAFFVLGTMGGAIFLSIIQHFSIPVDSIT 130

Qy     198 VALLIWNLGVVGMISIHWKG-PLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY 256
             :|::|  ::| :|:   | |: |:| |::::  ::|  | | ||||| | ||  :::|
Db     131 CFILLFNFTILGTLSVFAGGIPIVLRQCYMVVMGIVVAAWFTK-LPEWTTWFILVALALY 189

Qy     257 DLVAVLCPKGPLRMLVETAQERNETLFPALIY--------------SSTMVWLVN---- 297
           |||||| | |||::||| |  |:| | ||::|                |::  ||
Db     190 DLVAVLAPGGPLKLLVELASSRDEEL-PAMVYEARPTVSSGNQRRNRGSSLRALVGGGGV 248

Qy     298 MAEGDPEAQ----------RRVSKNSKYNAESTE--RESQDTVAENDDGGFSEE----- 339
             | | |           | | |  ||| :        | :     ||
Db     249 SDSGSVELQAVRNHDVNQLGRENSHNMDYNAIAVRDIDNVDDGIGNGSRGGLERSPLVGS 308

Qy     340 -WEAQRDSHLGPHRSTPESRAAVQELSSSILA-----GEDPEE--------------RG 378
            ::  : :|  |   | | :| :   | |      |:: ||               ||
Db     309 PSASEHSTSVGT-RGNMEDRESVMDEEMSPLVELMGWGDNREEARGLEESDNVVDISNRG 367

Qy     379 VKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPIS 438
           :|||||||||||||||:|   |  |  |  ||::||: ||  ||:||::: :||||||||
Db     368 IKLGLGDFIFYSVLVGRA---AMYDLMTVYACYLAIISGLGCTLILLSVYNRALPALPIS 424

Qy     439 ITFGLVFYFATDYLVQPFM 457
           |  |:|||| |  |::||:
Db     425 IMLGVVFYFLTRLLMEPFV 443


Search completed: March 14, 2003, 20:07:43
Job time : 27 secs
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 19:20:04 ; Search time 58 Seconds
(without alignments)
1659.035 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1984.5	83.0	468	13	Q90X08	Q90x08 gallus gall
2	1616	67.6	378	4	Q96P33	Q96p33 homo sapien
3	1612.5	67.4	456	13	Q9W6T7	Q9w6t7 brachydanio
4	1527.5	63.9	384	13	O73869	O73869 cyprinus ca
5	1473	61.6	289	4	Q9UIF0	Q9uif0 homo sapien
6	1445	60.4	448	11	Q91VS3	Q91vs3 mus musculu
7	1418	59.3	441	13	Q90ZE4	Q90ze4 brachydanio
8	1417	59.3	441	13	Q9I991	Q9i991 brachydanio
9	1370	57.3	504	5	Q8WS58	Q8ws58 branchiosto
10	1368.5	57.2	451	13	Q90X07	Q90x07 gallus gall
11	1362.5	57.0	525	5	Q8WS59	Q8ws59 branchiosto
12	1243.5	52.0	582	5	Q9GU38	Q9gu38 helix lucor
13	1221	51.1	261	11	Q91WK6	Q91wk6 mus musculu
14	1188	49.7	390	4	Q96P32	Q96p32 homo sapien
15	952.5	39.8	332	11	Q9D616	Q9d616 mus musculu
16	828.5	34.7	184	4	O95465	O95465 homo sapien
17	568	23.8	478	10	Q9SDG2	Q9sdg2 oryza sativ
18	539	22.5	397	10	Q9SIK7	Q9sik7 arabidopsis
19	153	6.4	291	17	Q8ZX12	Q8zx12 pyrobaculum
20	127.5	5.3	338	5	Q9GS14	Q9gs14 caenorhabdi
21	125.5	5.2	691	4	Q9HAS3	Q9has3 homo sapien
22	123.5	5.2	455	16	Q97FJ2	Q97fj2 clostridium
23	120.5	5.0	309	16	Q98QR5	Q98qr5 mycoplasma
24	118.5	5.0	305	4	Q96A60	Q96a60 homo sapien
25	117	4.9	224	2	Q8VSX2	Q8vsx2 staphylococ
26	115.5	4.8	339	17	O58554	O58554 pyrococcus
27	114	4.8	318	17	Q9HQ23	Q9hq23 halobacteri
28	114	4.8	417	16	Q8RH68	Q8rh68 fusobacteri
29	112	4.7	410	2	Q939W3	Q939w3 aeromonas s
30	111	4.6	705	11	Q8VIH3	Q8vih3 rattus norv
31	110.5	4.6	598	10	O82747	O82747 arabidopsis
32	110	4.6	601	5	Q95YF4	Q95yf4 drosophila
33	109	4.6	389	16	Q928L0	Q928l0 listeria in
34	108	4.5	291	16	Q98LC7	Q98lc7 rhizobium l
35	108	4.5	364	16	Q92UZ4	Q92uz4 rhizobium m
36	108	4.5	419	4	Q8TDV0	Q8tdv0 homo sapien
37	108	4.5	578	2	Q9RMN0	Q9rmn0 caulobacter
38	107.5	4.5	269	2	Q9WVX0	Q9wvx0 pediococcus
39	107	4.5	835	4	Q9ULF5	Q9ulf5 homo sapien
40	106.5	4.5	317	17	Q97CM0	Q97cm0 thermoplasm
41	105.5	4.4	699	10	Q93ZQ5	Q93zq5 arabidopsis
42	105	4.4	616	8	Q9G859	Q9g859 malawimonas
43	104.5	4.4	224	2	Q8VSX5	Q8vsx5 staphylococ
44	104	4.3	583	5	Q9VNZ5	Q9vnz5 drosophila
45	104	4.3	599	5	Q22089	Q22089 caenorhabdi

ALIGNMENTS

RESULT 1
Q90X08
ID Q90X08 PRELIMINARY; PRT; 468 AA.
AC Q90X08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Presenilin 1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E14; TISSUE=BRAIN;
RA Korade Mirnics Z., Keryanov S., Lovelock J., Corey S.J.;
RT "Cloning of chicken presenilins.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY043492; AAK95408.1; -.
DR InterPro; IPR001108; Presenilin.
DR Pfam; PF01080; Presenilin; 1.
DR PRINTS; PR01072; PRESENILIN.
SQ SEQUENCE 468 AA; 52812 MW; B746BEDA3BAC0BFA CRC64;

Query Match 83.0%; Score 1984.5; DB 13; Length 468;
Best Local Similarity 83.3%; Pred. No. 2.9e-157;
Matches 393; Conservative 29; Mismatches 41; Indels 9; Gaps 3;

```
Qy       1 MTELPAPLSYFQNAQMSE---DNHLSNTVRSQNDNRERQEH--NDRRSLGHPEPLSNGRP 55
           |||| | |  ||: ||:|   |||||||    ||| ||: |  ::||   :|   :||:|
Db       1 MTELSAHLPQFQHGQMTENFPDNHLSNT----NDNSERRRHDNSERRRNDNPGSETNGQP 56

Qy      56 QGNSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIY 115
           | | :|||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db      57 QNNIQQVVDQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIY 116

Qy     116 TPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLF 175
           |||||:|:|:|||||:||||||||||||:|||||||||||||||||| ||||||||||
```

```
Db    117 TPFTEETDTIGQRALNSILNAAIMISVIIVMTILLVVLYKYRCYKVIHGWLIISSLLLLF 176

Qy    176 FFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMAL 235
          ||||||||||||||||:||||||:||| |||||| ||||||||||||||||||||
Db    177 FFSFIYLGEVFKTYNVAMDYITVALIIWNFGVVGMICIHWKGPLRLQQAYLIMISALMAL 236

Qy    236 VFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWL 295
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    237 VFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAXERNETLFPALIYSSTMVWL 296

Qy    296 VNMAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTP 355
          ||||| ||| ||: |||| ||: ::   :||:  || ||||||:||: |||: :||  |||
Db    297 VNMAEEDPEGQRKASKNSTYDKQAPANQSQNEDAEADDGGFSQEWQQQRDNRIGPIESTP 356

Qy    356 ESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAIL 415
          ||||||| | |:    ||||||||||||||||||||||||||||||||||:|||||||
Db    357 ESRAAVQALPSNSQTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTLACFVAIL 416

Qy    416 IGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||| ||||||||||||||
Db    417 IGLCLTLLLLAIFKKALPALPISITFGLVFYFATDNLVQPFMDQLAFHQFYI 468


RESULT 2
Q96P33
ID   Q96P33      PRELIMINARY;      PRT;   378 AA.
AC   Q96P33;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Presenilin 1.
GN   PSEN1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kang L., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416717; AAL16811.1; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
SQ   SEQUENCE   378 AA;  42658 MW;  A09D6D2FC6F5618D CRC64;

  Query Match             67.6%;  Score 1616;  DB 4;  Length 378;
  Best Local Similarity   99.4%;  Pred. No. 1.2e-126;
  Matches  316;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQGALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAE 318
          ||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAE 318


RESULT 3
Q9W6T7
ID   Q9W6T7      PRELIMINARY;      PRT;   456 AA.
AC   Q9W6T7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Presenilin-1.
GN   PSEN.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Leimer U., Haass C.;
RT   "Expression, proteolytic processing, and amyloidogenic activity of
RT   zebrafish (Danio rerio) presenilin-1.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ132931; CAB40386.1; -.
DR   MEROPS; A22.001; -.
DR   ZFIN; ZDB-GENE-991119-4; psen.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
SQ   SEQUENCE   456 AA;  50981 MW;  B90C42280C874F8D CRC64;

  Query Match             67.4%;  Score 1612.5;  DB 13;  Length 456;
  Best Local Similarity   71.9%;  Pred. No. 3e-126;
  Matches  333;  Conservative   33;  Mismatches   78;  Indels   19;  Gaps    7;

Qy     12 QNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSRQVV-EQDEEED 70
          |||  :  |   :| | :        |:    | |       |     ||| : :|:||
Db      6 QNAANNVLNDGMDTSRHTSSTAAPPSRNEVELNGQP-------PTAPPPQVVTDSEEDED 58

Qy     71 EELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDG-QLIYTPFTEDTETVGQRA 129
          ||||||||||||||||:|||||||||||||||||||||:||| ||||||| ||||||||||
Db     59 EELTLKYGAKHVIMLFIPVTLCMVVVVATIKSVSFYTQKDGQQLIYTPFREDTETVGQRA 118

Qy    130 LHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTY 189
          |||:||| ||||||||||::|||||||||||| ||| |:|||||||| ||||||||||
Db    119 LHSMLNAIIMISVIVVMTLVLVVLYKYRCYKVIQAWLFFSNLLLLFFFSLIYLGEVFKTY 178

Qy    190 NVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLI 249
          |||:|| |:||:||| |||||| ||||||||||||||||||||||||||||||||||||
Db    179 NVAMDYFTLALIIWNFGVVGMICIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLI 238

Qy    250 LAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEAQRRV 309
          || |||||:|||||||||:|||||||||| :|||||||||||| |||:    |: |
Db    239 LAAISVYDLLAVLCPKGPLRILVETAQERNEAIFPALIYSSTMVWLFNMAD---SAETR- 294

Qy    310 SKNSKYNAESTERE---SQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSS 366
             || :     | :     |    |||||:  |   :   ||| :|| |||  :||: |
Db    295 -NNSSHPVPQQENQVVAMAPTAQAEDDGGFTPAWVDHQQHQLGPMQSTEESRRQIQEMPS 353

Qy    367 S--ILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTLLL 424
          :      :| ||||||||||||||:|||||||||||||||:|||||||||||||
Db    354 ARPPPPADDDEERGVKLGLGDFIFYSMLVGKASATASGDWNTTLACFVAILIGLCLTLLL 413

Qy    425 LAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||| ||:||||||| |||||
Db    414 LAIFKKALPALPISITFGLVFYFATDNLVRPFMDQLAVHQFYI 456


RESULT 4
O73869
ID   O73869      PRELIMINARY;      PRT;   384 AA.
AC   O73869;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
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```
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PS1 protein (Fragment).
GN   PS1.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337349; PubMed=9674592;
RA   Archer S., Hirano J., Diss J.K.J., Fraser S.P., Djamgoz M.B.A.;
RT   "Expression and localization in the fish retina of a homologue of the
RT   Alzheimer's related PS1 gene.";
RL   Neuroreport 9:2049-2056(1998).
DR   EMBL; Y17128; CAA76641.1; -.
DR   MEROPS; A22.001; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
FT   NON_TER       1      1
FT   VARIANT       5      5       I -> V.
FT   VARIANT      56     56       A -> S.
FT   VARIANT      56     56       A -> V.
FT   VARIANT      60     60       S -> G.
FT   VARIANT      63     63       V -> L.
FT   VARIANT      83     83       G -> A.
FT   VARIANT     118    118       A -> S.
FT   VARIANT     200    200       P -> T.
SQ   SEQUENCE   384 AA;  43276 MW;  F97EEFE24B31FDAA CRC64;

  Query Match             63.9%;  Score 1527.5;  DB 13;  Length 384;
  Best Local Similarity   79.3%;  Pred. No. 3e-119;
  Matches  310;  Conservative   28;  Mismatches   40;  Indels   13;  Gaps    6;

Qy      83 IMLFVPVTLCMVVVVATIKSVSFYTRKDG-QLIYTPFTEDTETVGQRALHSILNAAIMIS 141
           ||||:|||||||||||||||||||:||| ||||||| |||||||||||:|:||||||||
Db       1 IMLFIPVTLCMVVVVATIKSVSFYTQKDGQQLIYTPFREDTETVGQRALNSMLNAAIMIS 60

Qy     142 VIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALL 201
           ||||||::|||||||||||||  ||  |:|||||||||||||||||:|| |:|::
Db      61 VIVVMTLVLVVLYKYRCYKVIQGWLFFSNLLLLFFFSFIYLGEVFKTYNVAMDYFTLAVI 120

Qy     202 IWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAV 261
           ||| |||||| ||||||||||||||||||||||||||||||||||||| ||||||:||
Db     121 IWNFGVVGMICIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAAISVYDLLAV 180

Qy     262 LCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTE 321
           ||||||||:|||||||||| :|||||||||||||| |||:    |: |   || :    :
Db     181 LCPKGPLRILVETAQERNEPIFPALIYSSTMVWLFNMAD---SAEPR--NNSSHPV--PQ 233

Qy     322 RESQDTVA----ENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILAG-EDPEE 376
           :|:|| ||      |||||:  |  |:   ||| :|| :||  :||| |:     || ||
Db     234 QENQDAVAPTAQPEDDGGFTPAWVNQQQHQLGPMQSTEDSRREIQELPSARPPPVEDDEE 293

Qy     377 RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALP 436
           |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db     294 RGVKLGLGDFIFYSMLVGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALP 353

Qy     437 ISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||| ||:||||||| |||||
Db     354 ISITFGLVFYFATDNLVRPFMDQLAVHQFYI 384


RESULT 5
Q9UIF0
ID   Q9UIF0      PRELIMINARY;      PRT;   289 AA.
AC   Q9UIF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Presenilin 1 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99063792; PubMed=9847074;
RA   Sulston J.E., Waterston R.;
RT   "Toward a complete human genome sequence.";
RL   Genome Res. 8:1097-1108(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kozlowicz A., Pape K., Biewald T.;
RT   "The sequence of Homo sapiens PAC clone RP4-687K1.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Waterston R.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC004858; AAF19253.1; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
FT   NON_TER     289    289
SQ   SEQUENCE   289 AA;  33067 MW;  D503395A31C0EECB CRC64;

  Query Match             61.6%;  Score 1473;  DB 4;  Length 289;
  Best Local Similarity   99.7%;  Pred. No. 7.4e-115;
  Matches  288;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYS 289
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYS 289


RESULT 6
Q91VS3
ID   Q91VS3      PRELIMINARY;      PRT;   448 AA.
AC   Q91VS3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Presenilin 2.
GN   PSEN2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST TUMOR;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010403; AAH10403.1; -.
DR   MGD; MGI:109284; Psen2.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
SQ   SEQUENCE   448 AA;  49964 MW;  2ED1DE7AFC3E0581 CRC64;
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  Query Match             60.4%;  Score 1445;  DB 11;  Length 448;
  Best Local Similarity   64.4%;  Pred. No. 2.8e-112;
  Matches  300;  Conservative   43;  Mismatches   81;  Indels   42;  Gaps    8;

Qy       3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSL-GHPEPLSNGRPQGNSRQ 61
Db      24 ESPTSRSCQEGRPGPEDGESTAQWRTQESEEDCEEDPDRYACSGAP-----GRPSG---- 74

Qy      62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
Db      75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127

Qy     122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
Db     128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy     182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
Db     188 LGEVLKTYNVAMDYPTLFLAVWNFGAVGMVCIHWKGPLVLQQAYLIVISALMALVFIKYL 247

Qy     242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
Db     248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307

Qy     302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
Db     308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEAFEAPLPGYPG------------ 349

Qy     362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
Db     350 EEL-------EEEEERGVKLGLGDFIFYSVLVGKAAATGNGDWNTTLACFIAILIGLCLT 402

Qy     422 LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
Db     403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448


RESULT 7
Q90ZE4
ID   Q90ZE4      PRELIMINARY;      PRT;   441 AA.
AC   Q90ZE4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Presenilin-2.
GN   PS2.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jiang Y.-J., Davies A., Lewis J.;
RT   "The cloning and function of ps2 in zebrafish.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF178539; AAK61828.1; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
SQ   SEQUENCE   441 AA;  49132 MW;  B0080F2ABC7674BD CRC64;

  Query Match             59.3%;  Score 1418;  DB 13;  Length 441;
  Best Local Similarity   62.0%;  Pred. No. 4.9e-110;
  Matches  294;  Conservative   45;  Mismatches   75;  Indels   60;  Gaps    8;

Qy       2 TELPAPLSYFQNAQMS----EDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQG 57
Db      20 SESPTVPSYNQDNAMSLPQDTDSKRSGAVRSRSAS----------GSGDAGPV------- 62

Qy      58 NSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQ-LIYT 116
Db      63 -DRERADTPDGEEEELTLKYGAKHVIMLFIPVTLCMVVVVATIKSVSFYTEKSGQRLIYT 121

Qy     117 PFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFF 176
Db     122 PFEEDPNSVGQRLLNSVLNTLVMISVIVFMTIILVLLYKYRCYKFIHGWLILSSLMLLFW 181

Qy     177 FSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALV 236
Db     182 FSFMYLGEVFKTYNVAMDYPTLVMIIWNFGVVGMICIHWKGPLRLQQAYLIVISALMALI 241

Qy     237 FIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLV 296
Db     242 FIKYLPEWSAWVILGAISIYDLIAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWMV 301

Qy     297 NMAEG---DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRS 353
Db     302 GMADSNNPDSAGERRRSGGGVRTQEGVESEDDAPQAGR------RQYSAEEDLE------ 349

Qy     354 TPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVA 413
Db     350 ---------------------EDRGVKLGLGDFIFYSVLVGKAAAT-GGDWNTTLACFVA 387

Qy     414 ILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
Db     388 ILIGLCLTLLLLAIFKKALPALPISITFGLVFYFSTDNLVRPFMDSLAAHQYYI 441


RESULT 8
Q9I991
ID   Q9I991      PRELIMINARY;      PRT;   441 AA.
AC   Q9I991;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Putative presenilin2 homolog.
GN   PRE2.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lardelli M., McCarty R., Tamme R., Kortschak D.;
RT   "The function of presenilin2 in zebrafish embryogenesis.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ271795; CAB71930.1; -.
DR   MEROPS; A22.002; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
SQ   SEQUENCE   441 AA;  49169 MW;  BC720F2398E5F82A CRC64;

  Query Match             59.3%;  Score 1417;  DB 13;  Length 441;
  Best Local Similarity   62.9%;  Pred. No. 5.9e-110;
  Matches  299;  Conservative   44;  Mismatches   70;  Indels   62;  Gaps   10;

Qy       2 TELPAPLSYFQNAQMS----EDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQG 57
Db      20 SESPTVPSYNQDNAMSLPQDTDSKRSGAVRSRSAS----------GSGDAGPV------- 62

Qy      58 NSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQ-LIYT 116
Db      63 -DRERADTPDGEEEELTLKYGAKHVIMLFIPVTLCMVVVVATIKSVSFYTEKSGQRLIYT 121

Qy     117 PFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFF 176
Db     122 PFEEDPNSVGQRLLNSVLNTLVMISVIVFMTIILVLLYKYRCYKFIHGWLILSSLMLLFW 181

Qy     177 FSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALV 236
Db     182 FSFMYLGEVFKTYNVAMDYPTLLMIIWNFGVVGMICIHWKGPLRLQQAYLIVISALMALI 241

Qy     237 FIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLV 296
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```
          ||||||||:||:||  ||:|||:||||||||||||||||||||| :|||||||| |||:|
Db    242 FIKYLPEWSAWVILGAISIYDLIAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWMV 301

Qy    297 NMAEG---DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRS 353
          ||:    |   :|| |                ||     |     |  |
Db    302 GMADSNNPDSAGERRRS----------------------GGGVRTQEGVESEHDAP--- 335

Qy    354 TPESRAAVQELSSSILAGEDPEE-RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFV 412
              :|  :: |    | || || ||||||||||||||||||||:||  ||||||:||||
Db    336 ----QAGRRQYS----AEEDLEEDRGVKLGLGDFIFYSVLVGKAAAT-GGDWNTTLACFV 386

Qy    413 AILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          ||||||||||||||||||||||||||||||||:|| ||:|||| || ||:||
Db    387 AILIGLCLTLLLLAIFKKALPALPISITFGLVFYFSTDNLVRPFMDSLAAHQYYI 441


RESULT 9
Q8WS58
ID   Q8WS58      PRELIMINARY;      PRT;   504 AA.
AC   Q8WS58;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Presenilin.
GN   PS.
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21590369; PubMed=11733140;
RA   Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Albalat R.;
RT   "Characterization of the amphioxus presenilin gene in a high gene-
RT   density genomic region illustrates duplication during the vertebrate
RT   lineage.";
RL   Gene 279:157-164(2001).
DR   EMBL; AF369891; AAL40416.1; -.
DR   EMBL; AF369890; AAL40416.1; JOINED.
DR   InterPro; IPR000847; HTH_LysR.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
DR   PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SQ   SEQUENCE   504 AA;  55443 MW;  9C3794D0302859B4 CRC64;

  Query Match             57.3%;  Score 1370;  DB 5;  Length 504;
  Best Local Similarity   58.8%;  Pred. No. 5.8e-106;
  Matches  275;  Conservative   56;  Mismatches  101;  Indels   36;  Gaps    7;

Qy     27 RSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSRQVVEQDEEEDEELTLKYGAKHVIMLF 86
          |||       :  |||  |      |   |   :  | :|||| |:|||||||||||||
Db     46 RSQQIQENTPDGADRREAG-----DGGEDHGIRHR--EDEEEEDTEMTLKYGAKHVIMLF 98

Qy     87 VPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDTETVGQRALHSILNAAIMISVIVVM 146
          ||:||| |||||| |::||| |:| |||||| |:  :   :   |: | |||: ||:||
Db     99 APVSLCMAVVVATISSITFYTEKNGYLIYTPFHEEGASTASKVGDSLANGAIMVGVILVM 158

Qy    147 TILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNLG 206
          |: ||:|||||||| || |||:|||:||| |::|||||| : ||:  ||||:|:::|| |
Db    159 TVFLVILYKYRCYKFIHGWLILSSLMLLFLFAYIYLGEVLQAYNIPCDYITLAIVMWNFG 218

Qy    207 VVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKG 266
          |||: ||||||| |||||||:|||||||||||||:|| | ||  ||:|||||||||||
Db    219 AVGMVCIHWKGPLLLQQAYLIVISALMALVFIKYLPDWTTWFILGAISLYDLVAVLCPKG 278

Qy    267 PLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTERES-- 324
          ||::|||||||||| :|||||||||:| | ||: |||||::  |  |  |:   : :
Db    279 PLKVLVETAQERNEPIFPALIYSSTMMWFVGMADSDPEAKKKKKKKKKRRADGDPQAAGA 338

Qy    325 -QDTVAENDDGGFSEEWEAQR--DSHLGPHR---------STPESRAAVQELSSSILA-- 370
           |   ::|||  :|   |       |:|         :: ::| | | ||:  |:
Db    339 PAGAVGGEEEGGFGPDWNESRGFQPTRRPNRGGNASDASVNSEDARQAAQNLSNGRLSPS 398

Qy    371 ----------GEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLC 419
                     || |||||||||||||||||||||  ::|||||:||||||||||
Db    399 GNQQQQQQQMEEDEDEEERGVKLGLGDFIFYSVLVGKAS--SNGDWNTTLACFVAILIGLC 456

Qy    420 LTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||:| |||  || || | ||  | |:
Db    457 LTLLLLAIFKKALPALPISITFGLIFNFATANLVTPFTDALASQQVYV 504


RESULT 10
Q90X07
ID   Q90X07      PRELIMINARY;      PRT;   451 AA.
AC   Q90X07;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Presenilin 2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Korade Mirnics Z., Keryanov S., Lovelock J., Corey S.J.;
RT   "Cloning of chicken presenilins.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY043493; AAK95409.1; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
SQ   SEQUENCE   451 AA;  50496 MW;  534E6364C627E8B0 CRC64;

  Query Match             57.2%;  Score 1368.5;  DB 13;  Length 451;
  Best Local Similarity   60.3%;  Pred. No. 6.7e-106;
  Matches  282;  Conservative   46;  Mismatches   75;  Indels   65;  Gaps    8;

Qy      3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR-- 60
          | |   ||    | ||                || | |  |::             |:||
Db     25 ESPPVPSYQDGLQASE-------------TREAQTHRKRQT-------------GSSRSP 58

Qy     61 -QVVEQD-------------EEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFY 106
            | ::|              | |:||||||||||||||||||||:|||||||| ||
Db     59 NNVADEDASDSDVRVRESALENEEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFY 118

Qy    107 TRKDGQLIYTPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWL 166
          | |:||||||||:||| :|||| |:|:||  ||||||||||: |||||||||| || ||
Db    119 TEKNGQLIYTPFSEDTPSVGQRLLNSVLNTIIMISVIVVMTVFLVVLYKYRCYKFIHGWL 178

Qy    167 IISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYL 226
          |:|| :||| |::|||||| |||||:|| || |:||| | |||| |||||||:||||||
Db    179 ILSSFMLLFLFTYIYLGEVLKTYNVAMDYPTVILIIWNFGAVGMIRIHWKGPLQLQQAYL 238

Qy    227 IMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPAL 286
          ||||||| |||||||||:||:||  ||:|||:|||||||||||| ||||||| :||||
Db    239 IMISALMVLVFIKYLPEWSAWVILGAISIYDLIAVLCPKGPLRMLXETAQERNQPIFPAL 298

Qy    287 IYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDS 346
          |||| |:| | ||:  |:   :      ::||  |||:  : : :|
Db    299 IYSSAMIWTVGMAK--PDTAAKGQSQQAWDAED-ERENHSSTSHSD-----------SQ 343

Qy    347 HLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNT 406
           |      |     ::|:         : |||||||||||||||||||:|| ||||||
Db    344 ILDTRSPAPSHPITLEEM--------EEEERGVKLGLGDFIFYSVLVGKAAATPSGDWNT 395

Qy    407 TIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQ 454
          |:|  |||||||||||||:|||||||||||||||:|||:|| ||:
Db    396 TLAXXVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVR 443


RESULT 11
Q8WS59
ID   Q8WS59      PRELIMINARY;      PRT;   525 AA.
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AC   Q8WS59;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Presenilin.
GN   PS.
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21590369; PubMed=11733140;
RA   Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Albalat R.;
RT   "Characterization of the amphioxus presenilin gene in a high gene-
RT   density genomic region illustrates duplication during the vertebrate
RT   lineage.";
RL   Gene 279:157-164(2001).
DR   EMBL; AF369891; AAL40414.1; -.
DR   EMBL; AF369890; AAL40414.1; JOINED.
DR   InterPro; IPR000847; HTH_LysR.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
DR   PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SQ   SEQUENCE   525 AA;  57598 MW;  2B14CF77A80F07DE CRC64;

  Query Match             57.0%;  Score 1362.5;  DB 5;  Length 525;
  Best Local Similarity   56.6%;  Pred. No. 2.6e-105;
  Matches  277;  Conservative   56;  Mismatches   99;  Indels   57;  Gaps    8;

Qy      27 RSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSRQVVEQDEEEDEELTLKYGAKHVIMLF 86
           |||       :  |||  |       |   |   :  | :|||| |:|||||||||||||
Db      46 RSQQIQENTPDGADRREAG-----DGGEDHGIRHR--EDEEEEDTEMTLKYGAKHVIMLF 98

Qy      87 VPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDTETVGQRALHSILNAAIMISVIVVM 146
           ||:||| |||||| |::||| |:| |||||| |:  :   :   |: | |||: ||:||
Db      99 APVSLCMAVVVATISSITFYTEKNGYLIYTPFHEEGASTASKVGDSLANGAIMVGVILVM 158

Qy     147 TILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNLG 206
           |: ||:|||||||| || |||:|||:||| |::|||||| : ||:  ||||:|:::|| |
Db     159 TVFLVILYKYRCYKFIHGWLILSSLMLLFLFAYIYLGEVLQAYNIPCDYITLAIVMWNFG 218

Qy     207 VVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKG 266
           |||: ||||||| |||||||:|||||||||||||:|| | ||  ||:||||||||||
Db     219 AVGMVCIHWKGPLLLQQAYLIVISALMALVFIKYLPDWTTWFILGAISLYDLVAVLCPKG 278

Qy     267 PLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAES------- 319
           ||::|||||||||| :|||||||||:| | ||: ||||::  |  |  |:
Db     279 PLKVLVETAQERNEPIFPALIYSSTMMWFVGMADSDPEAKKKKKKKKKRRADGDPQAAGG 338

Qy     320 ---TERESQDT--------------VAENDDGGFSEEWEAQR--DSHLGPHR-------- 352
               : |:  |               |   ::|||  :|   |       |:|
Db     339 FRLLDNEAGSTGDDADAFDSAPAGAVGGEEEGGFGPDWNESRGFQPTRRPNRGGNASDAS 398

Qy     353 -STPESRAAVQELSSSILA-------------GEDPEERGVKLGLGDFIFYSVLVGKASA 398
           :: ::| | | ||:  |:                || ||||||||||||||||||||||
Db     399 VNSEDARQAAQNLSNGRLSPSGNQQQQQQMEEDEDEEERGVKLGLGDFIFYSVLVGKAS- 457

Qy     399 TASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMD 458
           ::||||||:|||||||||||||||||||||||||||||||||:| |||  || || |
Db     458 -SNGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLIFNFATANLVTPFTD 516

Qy     459 QLAFHQFYI 467
           ||  | |:
Db     517 ALASQQVYV 525


RESULT 12
Q9GU38
ID   Q9GU38      PRELIMINARY;      PRT;   582 AA.
AC   Q9GU38;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Presenilin.
GN   PS.
OS   Helix lucorum.
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Helicacea; Helicidae; Helix.
OX   NCBI_TaxID=31229;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Rogaev E.I., Riazanskaia N.N., Dvorianchikov G., Grigorenko A.P.,
RA   Tyrsin O.;
RT   "Presenilin gene isolated from mollusk Helix lucorum.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF197881; AAG28518.1; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
SQ   SEQUENCE   582 AA;  63782 MW;  07934E7C452199F0 CRC64;

  Query Match             52.0%;  Score 1243.5;  DB 5;  Length 582;
  Best Local Similarity   48.1%;  Pred. No. 2.5e-95;
  Matches  267;  Conservative   73;  Mismatches  108;  Indels  107;  Gaps   11;

Qy       9 SYFQNAQMSEDNHLSNTV--------RSQNDNRERQEHNDRRSLGHPEPLS------NGR 54
           | : : ||| :: : | |         ||| |   |   |: |     :  |      |
Db      39 SRYGSLQMSTEDDV-NAVPEATVVDPRSQGDASSRSAGNNSRHQVTSQARSERRAPPNTE 97

Qy      55 PQGNSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLI 114
           | | :     |||::||| || ||||||||||:|||||||||||||| |:::||     ||
Db      98 PSGGN-----QDEDDDEE-TLLYGAKHVIMLFIPVTLCMVVVVATISSITYYTSGGVYLI 151

Qy     115 YTPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLL 174
           |||| : ||  | :   |: || |:: |||||||::|::||||:||:||: ||:::||:||
Db     152 YTPFHDVTEDTGTKLWQSMANAVILLCVIVVMTVVLLLLYKYKCYRVINGWLVLSSIMLL 211

Qy     175 FFFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMA 234
           |||||:|| :: : ||  :||:|||:::|| || |:  ||||||| |||||||::|||:|
Db     212 FFFSFMYLEQILRAYNAPMDYVTVAIIMWNFGVGGLFCIHWKGPLLLQQAYLIVVSALVA 271

Qy     235 LVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVW 294
           |:|||| |:|| | :| |: ::|||||||||||||||||||| ||| :| ||||||||:|
Db     272 LMFIKYTPDWTTWAVLGVMVIWDLVAVLCPKGPLRMLVETAQSRNEPIFRALIYSSTMMW 331

Qy     295 LVNMAEGDPEAQRRVS-----KNSKYNAESTERESQDTVAENDDGGFSEEWE--AQRDSH 347
           | ||:   :::::       |    |:  |    :||  ::|||||:|       |
Db     332 PVTMADDGDQSKKKQKKKKGLKTGAQNSSVTTPLGKDT--DDDDGGFTEHVANGTNRQHS 389

Qy     348 LGPHRSTPESRAAVQEL------------------------SSSILAGED--------- 373
           |   : :  :| |||                           |: :|| :|
Db     390 LTASQDSQSARNAVQAFGDMVQDKPRTDRNAVSHTTVVNTTNSARVLATKDGAGVESAVR 449

Qy     374 ----------------------------------------PEERGVKLGLGDFIFYSVL 392
                                                    ||||||||||||||| ||
Db     450 VNVDQRDGAVVANSRSQNNSRTRPALQRRPLDSDSIDQDDSEEERGVKLGLGDFIFYGVL 509

Qy     393 VGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYL 452
           ||||| ::|||||:|||||||||| |||||||:|||||||||:|||||| |   |
Db     510 VGKAS--SNGDWNTTLACFVAILIGLCCTLLLLAIFRKALPALPISLTFGLVFNFATSSL 567

Qy     453 VQPFMDQLAFHQFYI 467
           |||||| ||  | ||
Db     568 VQPFMDSLASEQVYI 582


RESULT 13
Q91WK6
ID   Q91WK6      PRELIMINARY;      PRT;   261 AA.
AC   Q91WK6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to presenilin 1.
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GN   PSEN1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EYE, AND RETINA;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014744; AAH14744.1; -.
DR   MGD; MGI:1202717; Psen1.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
SQ   SEQUENCE   261 AA;  29849 MW;  16FB53FBE20EA4EB CRC64;

  Query Match           51.1%;  Score 1221;  DB 11;  Length 261;
  Best Local Similarity  91.8%;  Pred. No. 6.9e-94;
  Matches  235;  Conservative   14;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           |||:||||||||||||||:| |: :|||||::|||: :||: | :|||:|||||| |||
Db       1 MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQHDRQRLDNPEPISNGRPQSNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||:|||||||| ||||||:|||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYVTVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVY 256
           ||||||||||||||||
Db     241 LPEWTAWLILAVISVY 256


RESULT 14
Q96P32
ID   Q96P32      PRELIMINARY;      PRT;   390 AA.
AC   Q96P32;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Presenilin 2 transcript variant 2 (Fragment).
GN   PSEN2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Xu Y., Hu X., Zhou Y., Peng X., Yuan J., Qiang B.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416718; AAL16812.1; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
FT   NON_TER     390    390
SQ   SEQUENCE   390 AA;  43727 MW;  A62C791CED9DCF8A CRC64;

  Query Match           49.7%;  Score 1188;  DB 4;  Length 390;
  Best Local Similarity  62.0%;  Pred. No. 6.4e-91;
  Matches  253;  Conservative   35;  Mismatches   78;  Indels   42;  Gaps    8;

Qy       3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
           | | | |  :  |  ||   :   |||  :  : :|  ||    | |     ||| |
Db      24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP-----GRPPG---- 74

Qy      62 VVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                  :|||||||||||||||||||||:||||||||| ||| |:|||||| ||||
Db      75 -------LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTED 127

Qy     122 TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIY 181
           | :|||| |:|:||  |||||||||| |||||||||| || |||:|||:||| |::||
Db     128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187

Qy     182 LGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYL 241
           |||| ||||||:|| |: | :|| | |||: ||||||| ||||||||||||||||||||
Db     188 LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247

Qy     242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
           |||:||:|| ||||||||||||||||||||||||||| :|||||| | ||| | ||:
Db     248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYLSAMVWTVGMAKL 307

Qy     302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
           || :|  :     |: |  | :| |:  |     : | :|     : |
Db     308 DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------------ 349

Qy     362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA 409
           :||       |: ||||||||||||||||||:|| |||||||:|
Db     350 EEL-------EEEEERGVKLGLGDEIFYSVLVGKAAATGSGDWNTTLA 390


RESULT 15
Q9D616
ID   Q9D616      PRELIMINARY;      PRT;   332 AA.
AC   Q9D616;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   0 day neonate head cDNA, RIKEN full-length enriched library,
DE   clone:4833416A15, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=HEAD;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK014706; BAB29514.1; -.
DR   InterPro; IPR001108; Presenilin.
DR   Pfam; PF01080; Presenilin; 1.
DR   PRINTS; PR01072; PRESENILIN.
SQ   SEQUENCE   332 AA;  37588 MW;  5728A699675A7D4D CRC64;

  Query Match           39.8%;  Score 952.5;  DB 11;  Length 332;
  Best Local Similarity  72.0%;  Pred. No. 2.3e-71;
  Matches  190;  Conservative   22;  Mismatches   35;  Indels   17;  Gaps    3;

Qy      27 RSQNDNRERQEHNDRRSL-GHPEPLSNGRPQGNSRQVVEQDEEEDEELTLKYGAKHVIML 85
           |:|    : :|  || :  | |     ||| |            :|||||||||  ||||
```

```
Db     48 RTQESEEDCEEDPDRYACSGAP-----GRPSG-----------LEEELTLKYGANDVIML 91

Qy     86 FVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDTETVGQRALHSILNAAIMISVIVV 145
          ||||||||:|||||||| ||| |:|||||||||||| :|||| |:|:||  |||||||
Db     92 FVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVV 151

Qy    146 MTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNL 205
          ||| |||||||||| || |||:|||:||| |::|||||| |||||||:|| |: | :||
Db    152 MTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLFLAVWNF 211

Qy    206 GVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPK 265
          | |||: ||||||| |||||||:|||||||||||||||||:||:||  ||||||||||||
Db    212 GAVGMVCIHWKGPLVLQQAYLIVISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPK 271

Qy    266 GPLRMLVETAQERNETLFPALIYS 289
          |||||||||||||| :|||||||
Db    272 GPLRMLVETAQERNEPIFPALIYS 295

Search completed: March 14, 2003, 20:08:58
Job time : 70 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 19:14:13 ; Search time 38 Seconds
(without alignments)
1637.580 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2387	99.8	467	17	AAW05733	Presenilin-1-1. H
2	2387	99.8	467	19	AAW23964	Human presenilin-1
3	2387	99.8	467	19	AAW41430	PS1/467 protein.
4	2387	99.8	467	20	AAY24419	Human presenilin-1
5	2387	99.8	467	20	AAY23897	Amino acid sequenc
6	2387	99.8	467	21	AAB07971	Amino acid sequenc
7	2387	99.8	467	22	AAE10798	Human presenilin-1
8	2387	99.8	467	22	AAG63936	Amino acid sequenc
9	2387	99.8	467	22	AAE05466	Human presenilin (
10	2387	99.8	467	23	AAO18049	Presenilin protein
11	2387	99.8	467	23	AAU79416	Human presenilin-1
12	2387	99.8	467	23	AAE17051	Human mutant prese
13	2384	99.7	467	17	AAW05755	Presenilin-1-1 L28
14	2384	99.7	467	17	AAW05758	Presenilin-1-1 L39
15	2384	99.7	467	17	AAW05737	Presenilin-1-1 V82
16	2383	99.7	467	17	AAW05754	Presenilin-1-1 A28
17	2383	99.7	467	17	AAW05736	Presenilin-1-1 A79
18	2383	99.7	467	17	AAW05747	Presenilin-1-1 I23
19	2383	99.7	467	17	AAW05749	Presenilin-1-1 A26
20	2383	99.7	467	22	AAE05563	Human presenilin P
21	2382	99.6	467	17	AAW05738	Presenilin-1-1 V96
22	2382	99.6	467	17	AAW05739	Presenilin-1-1 Y11
23	2382	99.6	467	17	AAW05741	Presenilin-1-1 I14
24	2382	99.6	467	17	AAW05746	Presenilin-1-1 I21
25	2382	99.6	467	17	AAW05748	Presenilin-1-1 A24
26	2382	99.6	467	18	AAW27176	Human S182 gene, P
27	2381	99.6	467	17	AAW05753	Presenilin-1-1 E28
28	2381	99.6	467	17	AAW05757	Presenilin-1-1 G38
29	2381	99.6	467	17	AAW05740	Presenilin-1-1 M13
30	2381	99.6	467	17	AAW05742	Presenilin-1-1 M14
31	2380	99.5	467	17	AAW05744	Presenilin-1-1 L17
32	2380	99.5	467	19	AAW56770	Homo sapiens PS-1.
33	2380	99.5	467	22	AAE05564	Human presenilin P
34	2379	99.5	467	17	AAW05752	Presenilin-1-1 P26
35	2378	99.5	467	17	AAW05743	Presenilin-1-1 H16
36	2378	99.5	467	17	AAW05745	Presenilin-1-1 G20
37	2377	99.4	467	17	AAW05751	Presenilin-1-1 P26
38	2377	99.4	467	23	AAE17045	Human mutant prese
39	2376	99.4	467	17	AAW05759	Presenilin-1-1 C41
40	2375	99.3	467	17	AAW05750	Presenilin-1-1 C26
41	2375	99.3	467	23	AAE17046	Human mutant prese
42	2366	99.0	465	21	AAY51393	Human S182 protein
43	2366	99.0	467	18	AAW11839	Human early onset
44	2365	98.9	467	23	AAE17047	Human mutant prese
45	2361	98.7	463	17	AAW05734	Presenilin-1-2. H

ALIGNMENTS

RESULT 1
AAW05733
ID AAW05733 standard; Protein; 467 AA.
XX
AC AAW05733;
XX
DT 23-JUL-1997 (first entry)
XX
DE Presenilin-1-1.
XX
KW Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy.
XX
OS Homo sapiens.
XX
PN WO9634099-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX
DR WPI; 1996-497631/49.
DR N-PSDB; AAT40028.

```
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 2; Page 128-130; 178pp; English.
XX
CC   AAW05733 and AAW05734 represent the two different forms of wild type
CC   human presenilin-1 (PS-1). The form represented by AAW05734 results from
CC   alternate splicing of the genomic DNA sequence. AAW05762 represents the
CC   coding sequence for wild type human PS-2. The presenilins are a family
CC   of highly conserved integral membrane proteins with a common structural
CC   motif, common alternate splicing patterns, and common mutational hot
CC   spot regions. Mutations in PS genes are implicated in familial
CC   Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC   haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC   the DNA encoding these sequences can be used for diagnosis of these
CC   diseases. These proteins, or vectors that express them or containing
CC   antisense sequences, antibodies selective for mutant forms of these
CC   proteins (such as AAW05736) and modulators of PS gene expression are
CC   potentially useful for treatment of AD etc. Transgenic animals are useful
CC   as models for drug screening. The antibodies can also be used e.g. for
CC   affinity purification and in immunoassays.
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 17;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
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Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
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Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 2
AAW23964
ID   AAW23964 standard; Protein; 467 AA.
XX
AC   AAW23964;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human presenilin-1.
XX
KW   Presenilin-1; PS1 gene; human; familial Alzheimer's disease; FAD;
KW   cerebral haemorrhage; schizophrenia; depression; epilepsy;
KW   mental retardation; diagnosis; therapy; transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          82..100
FT                   /label= TM1
FT                   /note= "transmembrane domain 1"
FT   Domain          101..132
FT                   /label= TM1-2
FT                   /note= "hydrophilic loop"
FT   Domain          133..154
FT                   /label= TM2
FT                   /note= "transmembrane domain 2"
FT   Domain          155..163
FT                   /label= TM2-3
FT                   /note= "hydrophilic loop"
FT   Domain          164..183
FT                   /label= TM3
FT                   /note= "transmembrane domain 3"
FT   Domain          184..194
FT                   /label= TM3-4
FT                   /note= "hydrophilic loop"
FT   Domain          195..212
FT                   /label= TM4
FT                   /note= "transmembrane domain 4"
FT   Domain          213..220
FT                   /label= TM4-5
FT                   /note= "hydrophilic loop"
FT   Domain          221..238
FT                   /label= TM5
FT                   /note= "transmembrane domain 5"
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FT                   /label= TM5-6
FT                   /note= "hydrophilic loop"
FT   Domain          244..262
FT                   /label= TM6
FT                   /note= "transmembrane domain 6"
FT   Domain          263..407
FT                   /label= TM6-7
FT                   /note= "hydrophilic loop"
FT   Domain          408..428
FT                   /label= TM8
FT                   /note= "transmembrane domain 8"
FT   Misc-difference 177
FT                   /note= "Phe117Ser mutation site (Claim 1)"
FT   Misc-difference 439
FT                   /note= "Ile439Val mutation site (Claim 1)"
FT   Misc-difference 257
FT                   /note= "Asp257Ala mutation site, associated with
FT                          residue 258-290 deletion (Claim 1)"
FT   Misc-difference 258..290
FT                   /note= "residue 258-290 deletion mutant, associated
FT                          with Asp257Ala mutation (Claim 1)"
FT   Misc-difference 143
FT                   /note= "Ile143Thr mutation site (Claim 18)"
FT   Misc-difference 146
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FT   Misc-difference 171
FT                   /note= "Leu171Pro mutation site (Claim 18)"
FT   Misc-difference 260
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FT   Misc-difference 263
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FT   Misc-difference 264
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FT   Misc-difference 267
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FT   Misc-difference 280
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FT                   /note= "Glu280Gly mutation site (Claim 18)"
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FT   Misc-difference 384
FT                   /note= "Gly384Ala mutation site"
FT   Misc-difference 26..29
FT                   /note= "residue 26-29 deletion, resulting from
FT                         alternative splicing"
XX
PN   WO9801549-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;    97WO-CA00475.
XX
PR   02-JAN-1997;    97US-0034590.
PR   05-JUL-1996;    96US-0021673.
PR   12-JUL-1996;    96US-0021700.
PR   08-NOV-1996;    96US-0029895.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1998-286355/25.
DR   N-PSDB; AAV04666.
XX
PT   New isolated mutant presenilin-1 genes - useful for developing
PT   products for use in detection, diagnosis and therapy of Alzheimer's
PT   disease and for drug screening
XX
PS   Claim 1; Page 180-182; 238pp; English.
XX
CC   This polypeptide comprises human presenilin-1 (hPS1).  Its amino
CC   acid sequence was deduced from an isolated cDNA clone (see AAV04666).
CC   Another hPS1 sequence (see AAW23965) results from alternative
CC   splicing of the hPS1 mRNA transcript.  A murine PS1 homologue (see
CC   AAW23966) and a human presenilin-2 protein (see AAW23967) are also
CC   provided.  Mutations in the PS-1 and PS-2 genes are linked to the
CC   development in humans of forms of familial Alzheimer's disease
CC   (FAD) and may be causative of other disorders, e.g. cognitive,
CC   intellectual, neurological or physiological disorders such as
CC   cerebral haemorrhage, schizophrenia, depression, mental retardation
CC   and epilepsy.  Use of the nucleic acids and proteins comprising or
CC   derived from the presenilins is made in screening and diagnosing
CC   FAD, identifying and developing therapeutics for treatment of FAD,
CC   and in producing cell lines and transgenic animals useful as models
CC   of FAD.  Methods for identifying substances that bind to, or
CC   modulate the activity of a presenilin protein, and methods for
CC   identifying substances that affect the interaction of a
CC   presenilin-interacting protein with a presenilin protein are also
CC   disclosed.
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 19;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 3
AAW41430
ID   AAW41430 standard; Protein; 467 AA.
XX
AC   AAW41430;
XX
DT   04-JUN-1998  (first entry)
XX
DE   PS1/467 protein.
XX
KW   Presenilin peptide; PS1/429; immunogen; immune response; PS1 gene;
KW   Alzheimer's disease; mitochondrial pathology; neurodegeneration;
KW   apoptosis; PS1/467.
XX
OS   Homo sapiens.
XX
PN   WO9746678-A1.
XX
```

```
PD   11-DEC-1997.
XX
PF   03-JUN-1997;   97WO-US09272.
XX
PR   18-JUL-1996;   96US-0683315.
PR   06-JUN-1996;   96US-0659296.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Chisholm JC,  Davis JN,  Drache B;
XX
DR   WPI; 1998-042186/04.
DR   N-PSDB; AAV17358.
XX
PT   DNA encoding presenilin peptide PS1/429 and its analogues - useful
PT   for diagnosis and treatment of Alzheimer's disease
XX
PS   Claim 7; Fig 2; 77pp; English.
XX
CC   This sequence is the PS1/467 presenilin peptide. This sequence is
CC   specifically stated as not being in the nucleic acid of the invention,
CC   which encodes the PS1/429 presenilin peptide PS1/429 (II). Cells
CC   transformed with the DNA are used to produce recombinant (II) and
CC   analogues, useful e.g. as immunogens for generating an immune response
CC   against PS1/429. (II) is a new product of the PS1 gene, mutations in
CC   which cause Alzheimer's disease (AD). The nucleic acids are generally
CC   useful as probes for detection and quantification of PS1/429,
CC   particularly for diagnosis of AD, especially the target sequences that
CC   hybridise with probes are isolated for sequencing. Antibodies (Ab) can
CC   also be diagnosed at the protein level using Ab as immunoassay reagents.
CC   Ab can also be used to identify epitopes and for affinity purification of
CC   peptides. Antisense nucleic acid may also be used to regulate expression
CC   of the PS1/429 gene, and both nucleic acids and peptides are useful as
CC   size markers in electrophoresis, chromatography etc. The transgenic
CC   animals are used as models for AD, e.g. for testing drugs. Regulators of
CC   the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases
CC   involving mitochondrial pathology, apoptosis and neurodegeneration.
CC   Typical regulators are antisense sequences, ribozymes, aptamers,
CC   synthetic or natural compounds. (II) may also be used to target other
CC   coding sequences to particular cellular locations.
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 19;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 4
AAY24419
ID   AAY24419 standard; Protein; 467 AA.
XX
AC   AAY24419;
XX
DT   23-SEP-1999  (first entry)
XX
DE   Human presenilin-1.
XX
KW   Presenilin-1; mutation; gene mutant animal; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO9934670-A1.
XX
PD   15-JUL-1999.
XX
PF   07-JAN-1999;   99WO-JP00015.
XX
PR   08-JAN-1998;   98JP-0002191.
XX
PA   (DAUC ) DAIICHI PHARM CO LTD.
XX
PI   Takeda J,  Takeda M;
XX
DR   WPI; 1999-430307/36.
DR   N-PSDB; AAX90184.
XX
PT   Mutant presenilin-1 gene-introduced animals, useful as model animals
PT   for study of Alzheimer's diseases in human and screening substances
PT   for prevention and/or treatment of the diseases
XX
PS   Disclosure; Page 51-52; 64pp; Japanese.
XX
CC   The present invention describes a gene mutant animal having a non-human
CC   mutant presenilin gene. The mutant presenilin gene causes amino acid
CC   substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139,
CC   143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269,
CC   280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding
CC   N-terminals being e.g. A79V, V82L, A426 and P436S, particularly by
CC   replacing isoleucine of position 213 by another amino-acid especially
CC   threonine. The gene mutant animals e.g. mice can be used as model
CC   animals for the study of human Alzheimer's diseases and to screen and
CC   evaluate substances as candidates for prevention and/or therapy of
CC   Alzheimer's diseases in patients. They can over-produce amyloid
CC   beta protein by the presenilin-1 gene to cause nerve cell death or
CC   peeling off in the hippocampus earlier. Such animals are being
CC   pathologically close to human patients with Alzheimer's diseases. The
CC   present sequence represents human presenilin-1, as given in the present
CC   invention.
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 20;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
```

```
Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
```

RESULT 5
AAY23897
ID AAY23897 standard; protein; 467 AA.
XX
AC AAY23897;
XX
DT 27-SEP-1999 (first entry)
XX
DE Amino acid sequence of the wild type human presenilin 1 (PS1) protein.
XX
KW Human; presenilin 1; PS1; presenilin-binding protein; interacting domain;
KW presenilin allele; Alzheimer's disease; senile dementia;
KW psychiatric disease; schizophrenia; depression; neurological disease;
KW stroke; cerebral haemorrhage.
XX
OS Homo sapiens.
XX
PN WO9935501-A1.
XX
PD 15-JUL-1999.
XX
PF 08-JAN-1999; 99WO-CA00018.
XX
PR 09-JAN-1998; 98US-0070948.
XX
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, St George-Hyslop PH.
XX
DR WPI; 1999-419410/35.
XX
PT Identifying substances that alter presenilin interactions, useful
PT for screening individuals for presenilin alleles associated with
PT Alzheimer's disease - useful for diagnosis of Alzheimer's disease
XX
PS Disclosure; Page 34-36; 40pp; English.
XX
CC The present sequence represents wild type human presenilin 1 (PS1)
CC protein. The specification describes a method for identifying substances
CC that alter the interaction of a presenilin with a presenilin-binding
CC protein. The method comprises contacting the interacting domain of a
CC presenilin protein to a presenilin-binding protein in the presence of
CC a test substance, and measuring the interaction of the presenilin and
CC the presenilin-binding protein. The method can be used to screen
CC individuals for presenilin alleles associated with Alzheimer's disease
CC and related disorders, such as senile dementia's, psychiatric diseases
CC such as schizophrenia and depression, and neurological disease, such as
CC stroke and cerebral haemorrhage.
XX
SQ Sequence 467 AA;

Query Match 99.8%; Score 2387; DB 20; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
```

RESULT 6
AAB07971
ID AAB07971 standard; protein; 467 AA.
XX
AC AAB07971;
XX
DT 14-NOV-2000 (first entry)
XX
DE Amino acid sequence of human presenilin I polypeptide.
XX
KW Human; presenilin; PS1; PS2; nerve cell growth; nerve damage; hNPRAP;
KW neural plakophilin related armidillo protein; Alzheimer's disease;
KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; stroke;
KW multiple sclerosis; ischemia; stroke; neural paropathy; sciatic crush;
KW motor neuron disease; peripheral neuropathy; neuropathy; diabetes;
KW spinal cord injury; facial nerve crush.
XX
OS Homo sapiens.
XX
PN WO200047615-A2.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-CA00126.
XX
PR 12-FEB-1999; 99US-0119835.
XX
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
PI St George-Hyslop PH, Fraser PE;
XX
DR WPI; 2000-524531/47.
XX

PT Stimulation of nerve cell growth using human Neural Plakophilin Related
PT Armidillo Protein (hNPRAP) polypeptide, useful for the treatment of
PT diseases such as Alzheimer's, Parkinson's, and stroke -
XX
PS Disclosure; Page 19-20; 33pp; English.
XX
CC The present sequence represents a human presenilin I (PS1) polypeptide.
CC Human Neural Plakophilin Related Armidillo Protein (hNPRAP) polypeptide
CC is known to interact with PS1 and PS2. The specification describes a
CC method for stimulating the growth of nerve cells, comprising contacting
CC them with hNPRAP. The hNPRAP polypeptide and polynucleotide are useful
CC for treating nerve damage caused by a variety of diseases or physical
CC traumas, including Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis (ALS), multiple sclerosis, stroke, ischemia associated
CC with stroke, neural paropathy, motor neuron diseases, sciatic crush,
CC peripheral neuropathy, neuropathy associated with diabetes, spinal cord
CC injuries and facial nerve crush.
XX
SQ Sequence 467 AA;

Query Match 99.8%; Score 2387; DB 21; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
```

RESULT 7
AAE10798
ID AAE10798 standard; Protein; 467 AA.
XX
AC AAE10798;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human presenilin-1 (PS-1) protein.
XX
KW Human; catenin p120; presenilin-1; PS-1; neuroprotective; gene therapy;
KW neurodegenerative disease; Alzheimer's disease; nootropic; prophylaxis;
KW neuronal disorder; cognitive disorder.
XX
OS Homo sapiens.
XX

PN WO200167097-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-GB01059.
XX
PR 10-MAR-2000; 2000GB-0005895.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Hale RS, Rowley A, Blackstock W;
XX
DR WPI; 2001-589954/66.
DR N-PSDB; AAD18120.
XX
PT Identifying presenilin or catenin p120 activity modulator useful for
PT modulating presenilin-catenin p120 interaction and thus for treating
PT cognitive disorder e.g., Alzheimer's disease comprises enhancing
PT cognitive function -
XX
PS Example 1; Page 41-42; 48pp; English.
XX
CC The invention relates to a method for identifying modulators of
CC presenilin and catenin p120. Modulators of catenin p120 and presenilin
CC are useful for the treatment and prophylaxis of disorders that is
CC responsive to modulation of presenilin/catenin p120 activity. In
CC particular, neuronal disorders such as cognitive disorders and
CC neurodegenerative diseases such as Alzheimer's disease. Catenin p120 DNAs
CC are useful for identifying mutations in catenin p120 genes.
CC Identification of such mutations assist in the diagnosis of or
CC susceptibility to Alzheimer's or other conditions associated with
CC presenilin and in assessing the physiology of such disorders. Catenin
CC p120 DNAs are also used in hybridisation studies to monitor expression of
CC p120 genes and in particular for up or down regulation of catenin p120
CC expression. The present sequence is human presenilin-1 (PS-1) protein.
XX
SQ Sequence 467 AA;

Query Match 99.8%; Score 2387; DB 22; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
```

```
RESULT 8
AAG63936
ID   AAG63936 standard; Protein; 467 AA.
XX
AC   AAG63936;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Amino acid sequence of human presenilin 1.
XX
KW   KIAA0253; presenilin; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200167109-A1.
XX
PD   13-SEP-2001.
XX
PF   09-MAR-2001; 2001WO-GB01057.
XX
PR   10-MAR-2000; 2000GB-0005894.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Hale RS,  Rowley A,  Blackstock W;
XX
DR   WPI; 2001-522960/57.
DR   N-PSDB; AAH74993.
XX
PT   Identifying a modulator of presenilin function by determining the
PT   ability of presenilin to bind to a K1AA0253 polypeptide in the presence
PT   and absence of a test compound, useful in the treatment or prophylaxis
PT   of Alzheimer's disease -
XX
PS   Disclosure; Page 40-41; 48pp; English.
XX
CC   The present sequence represents human presenilin 1. KIAA0253 binds to
CC   presenilin. The specification describes a method of identifying a
CC   modulator of presenilin function or KIAA0253 function. The method
CC   comprises determining presenilin activity or KIAA0253 activity
CC   in the presence and absence of a test compound, where presenilin
CC   activity is determined by its ability to bind to KIAA0253. A modulator
CC   of presenilin or  K1AA0253 polypeptide is useful in the manufacture of
CC   a medicament for the treatment or prophylaxis of Alzheimer's disease.
CC   The K1AA0253 polynucleotide and K1AA0253 polypeptide are useful in the
CC   treatment, prophylaxis or diagnosis of Alzheimer's disease.
XX
SQ   Sequence   467 AA;

  Query Match           99.8%;  Score 2387;  DB 22;  Length 467;
  Best Local Similarity  99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 9
AAE05466
ID   AAE05466 standard; Protein; 467 AA.
XX
AC   AAE05466;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Human presenilin (PS1) protein.
XX
KW   Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;
KW   NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
KW   peripheral neuropathy; motorneuron disorder; neurodegenerative disorder;
KW   Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
KW   Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
KW   nerve deafness; Alzheimer's disease; epilepsy.
XX
OS   Homo sapiens.
XX
PN   WO200151671-A2.
XX
PD   19-JUL-2001.
XX
PF   08-JAN-2001; 2001WO-US00526.
XX
PR   10-JAN-2000; 2000US-0175200.
PR   04-JAN-2001; 2001US-0754949.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Mccarthy J,  Cordell B;
XX
DR   WPI; 2001-451872/48.
DR   N-PSDB; AAE05466.
XX
PT   Identifying inhibitors of neuronal degeneration useful for treating
PT   e.g. Alzheimer's disease, by determining the ability of a compound to
PT   induce nuclear factor kappa B activation, with the involvement of
PT   presenilin or Par-4  -
XX
PS   Claim 4; Page 60-61; 66pp; English.
XX
CC   The invention relates to human Par-4 protein, presenilin protein (PS1
CC   and PS2) and their corresponding DNA molecules. The invention also
CC   relates to a method for identifying inhibitors of neuronal degeneration,
CC   comprising cotransfecting eukaryotic host cells expressing presenilin
CC   (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct,
CC   exposing the cotransfected cells to a candidate molecule and monitoring
CC   the ability of the candidate molecule to induce NF-kappa B activation.
CC   Presenilin proteins participates in nuclear factor kappa B (NF-kappa B)
CC   signalling and activation. The inhibitors of neuronal degeneration
CC   are useful for treating neurodegenerative disorders such as Alzheimer's
CC   disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's
CC   chorea, Down's syndrome, nerve deafness, Meniere's disease and also for
CC   treating peripheral neuropathies, motorneuron disorders such as
CC   amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions
CC   involving spinal muscular atrophy and paralysis. The present sequence
CC   is human presenilin (PS1) protein.
```

```
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 22;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 10
AAO18049
ID   AAO18049 standard; Protein; 467 AA.
XX
AC   AAO18049;
XX
DT   02-SEP-2002  (first entry)
XX
DE   Presenilin protein.
XX
KW   Sel-12; presenilin; neuronal disorder; familial Alzheimer's disease;
KW   amyloid precursor protein; APP.
XX
OS   Unidentified.
XX
PN   US6376239-B1.
XX
PD   23-APR-2002.
XX
PF   04-APR-1997;   97US-0832867.
XX
PR   04-APR-1997;   97US-0832867.
XX
PA   (ELEG-) ELEGENE GMBH.
XX
PI   Baumeister R;
XX
DR   WPI; 2002-478281/51.
DR   N-PSDB; AAL47323.
XX
PT   Isolated DNA molecule comprising promoter of the sel-12 gene from
PT   Caenorhabditis elegans operably linked to heterologous gene, directs
PT   expression in neural cells and is useful to develop drugs to treat
PT   neuronal disorders -
XX
PS   Claim 2; Fig 4; 78pp; English.
XX
CC   The present invention relates to DNA molecules comprising the promoter of
CC   the sel-12 gene from Caenorhabditis elegans operably linked to a
CC   heterologous DNA sequence encoding a protein of interest. The sequence
CC   can be used to develop drugs for the treatment, prevention or delay of a
CC   neuronal disorder. In particular, the neuronal disorder may be familial
CC   Alzheimer's disease. The present sequence is a presenilin protein
CC   described in the exemplification of the invention.
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 23;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 11
AAU79416
ID   AAU79416 standard; protein; 467 AA.
XX
AC   AAU79416;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human presenilin-1, PS-1.
XX
KW   Human; integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB;
KW   gamma secretase; apoptosis; Alzheimer's disease; PS-1; nootropic;
KW   neuroprotective; cytostatic; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200222862-A2.
XX
PD   21-MAR-2002.
XX
PF   12-SEP-2001; 2001WO-GB04094.
XX
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PR   12-SEP-2000; 2000GB-0022333.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Hiles ID,  Ellis C;
XX
DR   WPI; 2002-351896/38.
XX
PT   Identifying agent that modulates interaction between integrin-linked
PT   kinase and presenilin-1, useful for treating Alzheimer's disease, and
PT   identifying agent that modulates protein kinase B or gamma secretase
PT   activity -
XX
PS   Disclosure; Page 43-45; 53pp; English.
XX
CC   The invention relates to identifying an agent modulating interaction
CC   between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising
CC   providing ILK, PS1 or their functional variants, as first and second
CC   components respectively, contacting the components in the presence of
CC   a test agent under conditions that in absence of the agent, would
CC   permit the components to interact and determining whether the agent is
CC   capable of modulating the interaction between the components. Also
CC   included are the method above where the components are protein kinase
CC   beta (PKB), gamma secretase or their functional variants, test kits
CC   for carrying out the methods and an agent identified by the methods.
CC   The methods are used for identifying an agent that modulates
CC   interaction between ILK and PS1. or PKB or gamma-secretase. The agent has
CC   therapeutic applications in treating humans or animals, for treating a
CC   host suffering from a condition associated with an interaction between
CC   ILK and PS1, activity of PKB, activity of gamma-secretase, apoptosis,
CC   cancer and Alzheimer's disease. The agent is also useful for
CC   manufacturing a medicament for use in treatment of the above mentioned
CC   conditions. The present sequence represents human presenilin-1, PS-1.
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 23;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
```

```
RESULT 12
AAE17051
ID   AAE17051 standard; Protein; 467 AA.
XX
AC   AAE17051;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human mutant presenilin 1 (PS1) wild type protein.
XX
KW   Human; presenilin 1; PS1; amyloid precursor protein; APP; drug screening;
KW   Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
KW   Huntington's disease; amylotrophic lateral sclerosis; Picks disease;
KW   head injury disease; frontal lobe dementia; cerebellar degeneration;
KW   ischaemic injury; schizophrenia.
XX
OS   Homo sapiens.
XX
PN   WO200202601-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US16508.
XX
PR   30-JUN-2000; 2000US-215345P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Carter DB,  Tomasselli AG;
XX
DR   WPI; 2002-140082/18.
XX
PT   Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT   useful for screening of drugs for treating pathologies associated with
PT   aberrant amyloid precursor protein processing, such as Alzheimer's
PT   disease -
XX
PS   Disclosure; Fig 1; 80pp; English.
XX
CC   The invention relates to mutant presenilin 1 (PS1) and presenilin 2
CC   (PS2) polypeptides. Presenilin are involved in the processing of amyloid
CC   precursor protein (APP) from which major amylodogenic peptides are
CC   cleaved. Mutant presenilins are useful for identifying agents that
CC   modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC   presenilin is also useful as a target for screening drugs useful in the
CC   treatment of pathologies associated with aberrant amyloid precursor
CC   protein processing, such as Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis,
CC   head injury disease, Picks disease, frontal lobe dementia, cerebellar
CC   degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC   non-human animal is useful for analysing the interaction between APP and
CC   mutant presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. A transgenic non-human
CC   animal is useful for analysing the interaction between APP and mutant
CC   presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. The present sequence is human
CC   PS1 wild type protein.
XX
SQ   Sequence   467 AA;

  Query Match             99.8%;  Score 2387;  DB 23;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-235;
  Matches  466;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
                ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
                |||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 13
AAW05755
ID   AAW05755 standard; Protein; 467 AA.
XX
AC   AAW05755;
XX
DT   23-JUL-1997  (first entry)
XX
DE   Presenilin-1-1 L286V mutation.
XX
KW   Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW   familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW   depression; antibody; gene expression modulator; therapy; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   286
FT                   /label= L286V
XX
PN   WO9634099-A2.
XX
PD   31-OCT-1996.
XX
PF   29-APR-1996;   96WO-CA00263.
XX
PR   31-JUL-1995;   95US-0509359.
PR   28-APR-1995;   95US-0431048.
PR   28-JUN-1995;   95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 3; Page -; 178pp; English.
XX
CC   AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC   protein (see AAW05733 for wild type sequence). AAW05734 represents a
CC   different wild type form of presenilin-1 that results from alternate
CC   splicing of the genomic DNA sequence. The presenilins are a family of
CC   highly conserved integral membrane proteins with a common structural
CC   motif, common alternate splicing patterns, and common mutational hot
CC   spot regions. Mutations in PS genes are implicated in familial
CC   Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC   haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC   the DNA encoding the wild type sequences can be used for diagnosis of
CC   these diseases. The wild type proteins, or vectors that express them or
CC   containing antisense sequences, antibodies selective for these mutant
CC   forms of the proteins and modulators of PS gene expression are
CC   potentially useful for treatment of AD etc. Transgenic animals are
CC   useful as models for drug screening. The antibodies can also be used e.g.
CC   for affinity purification and in immunoassays.
XX
SQ   Sequence   467 AA;

  Query Match             99.7%;  Score 2384;  DB 17;  Length 467;
  Best Local Similarity   99.6%;  Pred. No. 9.2e-235;
  Matches  465;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy    181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
          ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db    241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPAVIYSSTMVWLVNMAE 300

Qy    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
          |||||||||||||||||||||||||||||||||||||||||||||
Db    421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467


RESULT 14
AAW05758
ID   AAW05758 standard; Protein; 467 AA.
XX
AC   AAW05758;
XX
DT   23-JUL-1997  (first entry)
XX
DE   Presenilin-1-1 L392V mutation.
XX
KW   Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW   familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW   depression; antibody; gene expression modulator; therapy; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   392
FT                   /label= L392V
XX
PN   WO9634099-A2.
XX
PD   31-OCT-1996.
XX
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PF   29-APR-1996;   96WO-CA00263.
XX
PR   31-JUL-1995;   95US-0509359.
PR   28-APR-1995;   95US-0431048.
PR   28-JUN-1995;   95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 3; Page -; 178pp; English.
XX
CC   AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC   protein (see AAW05733 for wild type sequence). AAW05734 represents a
CC   different wild type form of presenilin-1 that results from alternate
CC   splicing of the genomic DNA sequence. The presenilins are a family of
CC   highly conserved integral membrane proteins with a common structural
CC   motif, common alternate splicing patterns, and common mutational hot
CC   spot regions. Mutations in PS genes are implicated in familial
CC   Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC   haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC   the DNA encoding the wild type sequences can be used for diagnosis of
CC   these diseases. The wild type proteins, or vectors that express them or
CC   containing antisense sequences, antibodies selective for these mutant
CC   forms of the proteins and modulators of PS gene expression are
CC   potentially useful for treatment of AD etc. Transgenic animals are
CC   useful as models for drug screening. The antibodies can also be used e.g.
CC   for affinity purification and in immunoassays.
XX
SQ   Sequence   467 AA;

  Query Match             99.7%;  Score 2384;  DB 17;  Length 467;
  Best Local Similarity   99.6%;  Pred. No. 9.2e-235;
  Matches  465;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120

Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVVVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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RESULT 15
AAW05737
ID   AAW05737 standard; Protein; 467 AA.
XX
AC   AAW05737;
XX
DT   23-JUL-1997  (first entry)
XX
DE   Presenilin-1-1 V82L mutation.
XX
KW   Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW   familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW   depression; antibody; gene expression modulator; therapy; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   82
FT                   /label= V82L
XX
PN   WO9634099-A2.
XX
PD   31-OCT-1996.
XX
PF   29-APR-1996;   96WO-CA00263.
XX
PR   31-JUL-1995;   95US-0509359.
PR   28-APR-1995;   95US-0431048.
PR   28-JUN-1995;   95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 3; Page -; 178pp; English.
XX
CC   AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC   protein (see AAW05733 for wild type sequence). AAW05734 represents a
CC   different wild type form of presenilin-1 that results from alternate
CC   splicing of the genomic DNA sequence. The presenilins are a family of
CC   highly conserved integral membrane proteins with a common structural
CC   motif, common alternate splicing patterns, and common mutational hot
CC   spot regions. Mutations in PS genes are implicated in familial
CC   Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC   haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC   the DNA encoding the wild type sequences can be used for diagnosis of
CC   these diseases. The wild type proteins, or vectors that express them or
CC   containing antisense sequences, antibodies selective for these mutant
CC   forms of the proteins and modulators of PS gene expression are
CC   potentially useful for treatment of AD etc. Transgenic animals are
CC   useful as models for drug screening. The antibodies can also be used e.g.
CC   for affinity purification and in immunoassays.
XX
SQ   Sequence   467 AA;

  Query Match             99.7%;  Score 2384;  DB 17;  Length 467;
  Best Local Similarity   99.6%;  Pred. No. 9.2e-235;
  Matches  465;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60

Qy      61 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
           |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db      61 QVVEQDEEEDEELTLKYGAKHLIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
```

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Qy     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180

Qy     181 YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     181 YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240

Qy     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300

Qy     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360

Qy     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420

Qy     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
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Search completed: March 14, 2003, 19:21:13
Job time : 40 secs